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AX747274 Sequence
AX01952 Homo sapi
BC033143 Homo sapi
AX535029 Sequence
AX535090 Sequence
CQ117675 Sequence
AL556390 Human DNA
AL592304 Homo sapi
BC006890 Mus muscu
BC079148 Rattus no
AL627228 Mouse DNA
AC095979 Rattus no
AC118963 Rattus no
AC126312 Rattus no
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                                                                     March 11, 2006, 19:43:27 ; Search time 8477 Seconds (without alignments) 11486.709 Million cell updates/sec
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Direct Submission
Direct Submission
Direct Submission
Submitted (04-JUL-2022) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
Kernalisenomice@hri.co.jp, Tel:81-438-52-396)
NEDO human cDNA sequencing project supported by Ministry of
Bconomy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trainslation="MERPGHPRASGPPRIGPWERPTELCLETYDKPPOPPBRRTRR
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Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomuza, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21, 243 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCCCCGCCCTGGACACCCCCCCCCCCAGCATCTGGGCCTCCACGCTTGGGACCCGTGGGAG
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Pred. No. 0;
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                                                                                                                                               Nat. Genet. 36 (1), 40-45 (2004) 14702039
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Best Local Similarity 99.9%;
Matches 1694; Conservative 0
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                                                                                                                                  human cDNAs
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us-09-989-890-105.rge

Submitted (25-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Preparation: Rubin Laboratory CDNA Library Preparation: Rubin Laboratory CDNA Library Preparation: Rubin MA.A.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@beggsc.bc.ca Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Mokea, Johnson Pang, Diana Mah, Jing Wang, Kieth Pichter, Eric Chuah, Allen Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Corto Duana Gmailing Jeth Randam, Jana Palmquist, JR	Glone distribution MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 43 Row: C Column: 17. Source /organism="Homo sapiens" / maje.rlp. / mage.llnl.gov / maje.rlp.	Clone Tib="NIH MGC 21" Clone Tib="Vector: pOTB7" Clone Start="Clotf172" Clotf172" Clotf172"
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Db 1634 GGATCTACGTTGCATCCCCAGCTGCTCCAGGCCCCTTCCTT	RESULT 7 CQ717675 1197 bp DNA linear PAT 03-FEB-2004 LGCUS CQ717675 EB-2004 DEFINITION Sequence 3609 from Patent W002068579. ACCESSION CQ717675. GI:42278532 VERSION CQ717675.1 GI:42278532 SOURCE Homo sapiens (human) ORGANISM Homo sapiens	JOURNAL Patent: WO 02068579-A 3609 06-SEP-2002; PEATURES Location(Qualifiers Location/Qualifiers 1. 1197 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 69.9%; Score 1197; DB 6; Length 1197; Best Local Similarity 100.0%; Pred. No. 4.1e-282; Anatches 1197; Onservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ATGCCCGCCTGGACACCCCGGCCAGCATCTGGGCCTCCAGGTTGGGACGTGGGAG 60 Db 1 ATGCCCGCCTGGACACCCCGCCCAGCATCTGGGCCTCCAGGTTGGGACCGTGGGAG 60	Oy 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCACCAAGCCGC 120	181 ATCTCTGGCTGCTGGCCGGCCCTTGAGTCCCCCCACCTGCTGCTGCTGCGCGACCC 241 TGGGTGTGGGAGTGGTGCCGGGCTGCCTTCCGCCGCGGGGTTGCCTCCAGGTGCTGCGGGGCTGCTGCTTCCGCCGGGGTTGCCTCCAGGTGGTGGCGGGGGTGCCTGCTTCTGCTTCCGCCGGGGTTGCCTCCAGGTGGCGGGGGTGCCTGCGGGGTTGCTTCTGCTTCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL356390 140207 bp DNA linear PRI 18-MAY-2005 Human DNA sequence from clone RP11-344H11 on chromosome 1 Contains the NR0B2 gene for nuclear receptor subfamily 0 (group B, member 2), the 5' end of a novel gene (FL12455), the NUDC gene fornuclear distribution gene C homolog (A. nidulans), a novel gene (FL134633), a ribosomal protein L12 (RPL12) pseudogene, a ribosomal protein L32 (RPL32) pseudogene, a novel genes and two CDG islands, complete sequence.

AL356390
AL356390.24 GI:21436506
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ACCESSION VERSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82239 ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTCTGGCGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 recensives constructed and reconstructed and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTCTGGCGACCC
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                                                                                                      Ġ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 140207;
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Pred. No. 1.9e-243;
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Matches 1039; C
                                                                                               misc_feature
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GLLKYCHLLVRGFRPRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLBRAHFGGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (50415. .50811)
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Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 110287 bases at least Q40
Consensus quality: 110500 bases at least Q20
Insert size: 111138; sum-of-contigs
Insert size: 119403; 8.4% error; agarose-fp
Quality coverage: 11.23x in Q20 bases; sum-of-contigs Quality
coverage: 10.67x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 1.2e-242;
0; Mismatches 2; Indels 0; Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 18058: contig of 18058 bp in length 18159; gap of 100 bp 18159; 35144: gap of 100 bp 18159; 35144: gap of 100 bp 18159; 35144: gap of 100 bp 18159; 35170: contig of 19466 bp in length 1811 72936: contig of 18126 bp in length 1813 5288: gap of 100 bp 18128 bp in length 1813 5288: gap of 100 bp 1852 bp in length 1813; contig of 1852 bp in length 18140: long and length 18159: contig of 1851 bp in length 18140: long and liny and liny
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fragment chain:I"

54811. .72936
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/clone_lib="RPCI-3"
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vector_side:right"
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Best Local Similarity 99.8%;
Matches 1037; Conservative (
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Homo sapiens chromosome 1 clone RP3-426N7, 7 unordered pieces.
AL592304
GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT 420
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                               Direct Submission
Submitted (24-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                      82419 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCAGCCCTGATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT
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Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL592304.1 GI:14586390
HTG; HTGS_PHASE1; HTGS_CANCELLED
HOmo gapiens (human)
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TCTGGCCTCAGCCAGGACGAGGCTGACAGTCCCCAGGAGACAACCGCAGATGCC 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC079148 1718 bp mRNA linear ROD 15-SEP-2004 Rattus norvegicus similar to hypothetical protein FLJ34633, mRNA (CDNA clone MGC:94165 IMAGE:7128510), complete cds.
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buerow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Wockernan, K.J., Malek, J.A., Gunarathe, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
                                                                                                                                                                                                    AGCATCACGCAGGACTACCACCTGGATGAGCAAGACGCCGAGGGCCGCCTGGTGCGGGGC 950
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MGC.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Busaryotas, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontogiires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Ruttus.
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                                                                 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC
                                                                                                         AAGTGCACATCGGACACCGTGTTCCTGGAGAAGACCAGCAAGATCTCAGACCTGATCAGC
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/translation="MSAPSPHRAVAPGGGTLRTLATMGGRVSPSFQALQNQPTSPQPA
/translation="MSAPSPHRAVAPGGGTLRTLATMGGRVSPSFQALGNQPTSPQPA
SKGAPGWGTGGUEDSASAAAGIAGSAYGLVGGAAPAPYLPETPETLKGETPRPPGPRUTM
VCPPARTVHPPAAGNKGSRPAMAAASATLMLSSKASLSTFTAMPPPGSLTWPPAARS
PWPSLLPHGTACLAPSPTAPAALRSTTPSMNRTWTCLRWAVAPCRAGRSTCLFSRS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                56.2%; Score 962.8; DB 9;
.larity 82.3%; Pred. No. 9.5e-225;
Conservative 0; Mismatches 232;
                                                                                                                              142. .792
/gene="1810019J16Rik"
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ETMVGSGLSQDELTVQISQETTADAIARKLRPYGAPGYPASQDSSPQGTDTDSSGAPL
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakeeley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Schern, J. S., Krzywinski, M. I., Skalska, U., Smailus, D. E., Scherch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15, 000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: (Dickson, Mark) mcdGapaxil.stanford.edu
Contact: (Dickson, Mark) mcdGapaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                         Direct Submission
Submitted (02-MGG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: d Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="similar to hypothetical protein FLJ34633"
/protein_id="AAH79148.1"
/db_xref="GI:50927713"
                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
//organism="Rattus norvegicus"
//db twef="Ratman"
//db xref="Ratman"
/clone="MGC:94165 IMAGE:7128510"
//clone="MGC:94165 IMAGE:7128510"
//clone lib="Rathangy, rat (Brown Norway)"
//lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Vector: pExpressl"
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/db_xref="GeneID:313018"
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                                                                                                                                                                                                                                                      Director MGC Project.
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TITLE
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COMMENT
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ATGCCCCGCCCTGGACACCCCCCCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG

12;

Indels

Score 935.8; DB 9; Pred. No. 3.9e-218; 0; Mismatches 267;

54.6%; ilarity 80.4%; Conservative

Similarity

Best Local Sim Matches 1148; Query Match

Length 1718;

1020 1080 1209 1032 1089 840 960 540 780 912 900 972 180 252 240 312 300 372 CGCTGTGGGGCCTGTGTGCGGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG 360 432 420 492 480 552 612 900 672 099 732 720 792 852 1090 TCTGGCCTCAGCCAGGATGAACTGACAGTGCAGATCTCCCAAGAGACAACAGCGCAGATGCC ATTICAGGCTCTGCAGAACCAGCCAACGAGCCCCCAACCTGCTGCCTCTGGCGCCCCC TGGGTGTGGGAGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG 313 TGGGGTTGGGACTGGTGTAGGGCTGCCTTCTGCTTCCGACGCTGCAGGGATTGCCTCCAG GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCCAGCCCTGATCGT TACCCCGATGTTAAGCTCCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA 841 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGC 901 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA 961 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGC 1021 TCAGGTCTCAGCCAGGATGAGCTGACAGATCTCCCAGGAGACGACTGCAGATGCC ATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCACCAAGCCGC 133 AGGCCCACAGAGTTATGCCTGGAAACGAATGATGAGGCGCTCCCAGCCCCCACCAGGCCGT GAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT GTGCTTATTTTCAAGAAGCTGACAGAGCTGTTCAGTGTACATCAGATTTAGACGAGCTGGCC 781 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC GCACCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCTTCAGC GCACCCCCCAGCCGCCGGGATGGCCAAAAGCTCAAGACCAGCATGGGCAGCTTCAGC AGCCTGCCCAGCACCTTTGCCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC 1081 셤 ð ò

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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNFEP; Information on the WORNFEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly the characteristic or the vertication digest, except on the rare occasion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VECTOR: pBACe3.6
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
                                                                                                                                                                                                                                                                                                       TITIGITG-----AATGATCCTAGACCACATACATITCACAGGCCCATGGCGCCCCACA-- 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2003
4, complete
                    TTCCAGGGCACGGACACAGACTCTTCAGGTGCACCCCTGCTGCAGGTGTACTGCTAACCC 1269
                                                                  CTGCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGGG 1260
                                                                                                                                                                                                AGGACCTCTGTGTGCAGGCCAGATTCTGAGCCCAGAAGAGAGTGACCTCTCTGGCTTGTGC 1387
                                                                                                                                                                                                                                                                   TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1380
                                                                                                                   --TCCTGACCCAGCAAGAGTCCCTCTTGGAAGAAGCATTAGCCAGCGGAGGAGGAACC 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 193813)
Hopkins, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-FEB-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 159, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests.clonerequestger.ac.uk on Reb 4, 2003 this sequence version replaced gi:22474404.
                                                                                                                                                                    1261 GGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the clone being a YAC.
RP23-137L22 is from the RPCI-23 Mouse BAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL627228 193813 bp DNA linear ROD Mouse DNA sequence from clone RP23-137L22 on chromosome
                                                                                                                                                                                                                                                                                                                                                                  1441 Trcrrcarrcracracrasarraacracrascrascrasscrasscrattra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (house mouse)
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SOURCE
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AUTHORS
TITLE
JOURNAL
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from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103949 AGGCCATCAGAGTTATGCCTGGAAACGAACGATGAGCGCTCCCAGCCCCACCGGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCACCCGTAGACCCACCCCAAGGACCCTGGCCACCATGGGCCCAGAGAGCATTACCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCACCCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA
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0; Mismatches 145;
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                                                                      1. 193813
/organism=Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="#"
/clone="RR23-137L22"
/clone_lib="RRC1-23"
                                                                                                                                                                                                                                                                                                   Score 791;
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al Similarity 85.8%;
891; Conservative C
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Direct Submission

Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

on Nov 9, 2002 this sequence version replaced gi:22772470.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Mithin each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence contigs within a contigs-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence crads. Both end sequences and whole genome shotgun sequence crads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: project information
Center project name: CH230-11020
Center clone name: CH230-11020
Center clone name: CH230-11020
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 227458 bases at least Q40
Consensus quality: 228649 bases at least Q30
Consensus quality: 228649 bases at least Q30
Consensus quality: 228649 bases at least Q30
Consensus quality: 228649 bases; at least Q20
Estimated insert size: 235033; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: Estimated insert size may differ from sequence length

* NOTE: This is a "vorking draft' sequence. It currently

* NOTE: This is a "vorking draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.

Subract Subrission

Submitted (17-5EP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

Rat Genome Sequencing Consortium.
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wieght, D., Wright, R., Wo, J., Yakub, S., Yen, J., Yoon, J., You, Y., Zhou, X., Zhou, X., Zhou, X., Zhou, X., Zhou, X., Zhou, X., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiss, G., Grien, G., G
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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/note="clone_boundary
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                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 235419)
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Rattus morvegicus (Norway rat)

Rattus morvegicus (Norway rat)

Rattus morvegicus (Metazoa; Chordata; Carniata; Vertebrata; Euteleostomi; Metazoa; Chordata; Muridae; Muridae; Murinae; Rattus

1 (Dagaathi; Muroides; Muridae; Murinae; Rattus

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              104789 ATCATCCGTATTAGTACCCGCAAAAGCCGCTCCCGCCCACAGACCTCCGAGGGCGCTCA 104848
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Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
unordered pieces.
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Rattus norvegicus (Norway rat)
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/estimated_length=unknown
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                                                                                                                                                                                                                                                                                                    Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.
On Nov 15, 2002 this sequence version replaced gi:23269749.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* CONSIS: This is a "working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Yon Niederhausern, A., Weiss, R., Smith, D. R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                             Direct Submission
Submitted (22-APR-2002) Human Genome Sequencing Center, Departmen
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Pred. No. 2.2e-178;
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-180E4"
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Rat Genome Sequencing Consortium
Direct Submission
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84.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCCTGCTGTCTACTGAGGACTCCACTGAG 360
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                                                                                                                                                                                                        61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTGTTGGCGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   841 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGC
1 ATGCCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG
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misc_feature
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                                                                                                                                                                                                                                                                                           Bakaryota, Metazoa Chordata, Craniata, Vertebrata, Buteleostomi, Mandia, Eutheria, Buarchontoglises, Gilres, Rodentia; Sciutognathi, Muridae, Murinae; Rattus.

Sciutognathi, Muridae, Murinae; Rattus.

1 (loasea 1 to 25601)

Sciutognathi, Muridae, Murinae; Rattus.

Aubrooks, L., Amartunge, H.C., Are, J.R., Ayele, M., Banks, T., Barberia, J., Benton, J., Bainge, K., Blankenburg, K., Bonnin, D., Bancok, J., Benton, P., Binge, K., Blankenburg, K., Bonnin, D., Bancok, J., Bowle, S., L., Amartunge, H.C., Mre, J.R., Byrd, N.C., Cher, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Carter, M., Caracos, S. R., Chacko, J., Chavez, D., Chen, G., Cox, C., Coyle, M.D. Dathorne, S. R., David, R., Delado, O., Denn, A.L., Ding, Y. Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durchin, K.J., Dolador, M., Bolado, O., Denn, A.L., Ding, Y. Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durchin, K.J., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durchin, K.J., Douthwaite, K.J., Chevara, W., Garrer, T., Garza, N., Gill, R., Gao, J., Garcia, A., Hogge, M., Halloway, C., Bull, H.H., Gao, J., Garcia, A., Hogge, M., Halloway, C., Hollins, B., Harris, C., Harris, K., Harr, M., Havlak, P., Hawe, M., Hamiton, K., Kattovic, J. Jia, Y., Lidhar, J., Hulber, S., Hume, J., Jackson, L. E., Jacobson, B., Kally, S., Khan, U., King, J., Lidhe, S., Hamiton, K., Marcin, M., Lidha, J., Lichtarge, O., Lieu, C., Liu, J., Lidha, J., Lidhar, S., Martina, R., Marin, R., Marin, R., Marin, R., Marin, R., Marin, M., Morkerson, J., Muchin, M., Morkerson, J., Newtson, M., Morgan, M., Morgan, M., Morkerson, E., Machen, P., Picken, R., Pace, A., Payton, B., Tamerisa, K., Marin, P., Picken, R., Pace, A., Payton, M., Sodergren, S., Sott, G., Taylor, T., Taleria, B., Lew, R., Marin, R., Marin, R., Wang, C., Wang, Y., Wang, R., Wang, C., Wang, W., Walliams, C., Willamson, M., Willerson, S., Warling, M., Walliams, C., Williams, C., Williams, C., Williams, C., Walliams, C., Walliams, C., Walliams, C., Walliams, C., Walliams
                                                              AC126312 256017 bp DNA linear HTG 13-NOV-2002
Rattus norvegicus clone CH230-1B9, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 13, 2002 this sequence version replaced gi:23267435. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas
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                                                                                                                                                                                AC126312.4 GI:24941465
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Direct Submission
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                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                          LOCUS
DEFINITION
                                AC126312/c
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JOURNAL
RESULT 15
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COMMENT

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(http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGCCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 83721: contig of 83721 bp in length
2 83821: gap of unknown length
2 253567: contig of 165746 bp in length
8 25367: gap of unknown length
8 256017: contig of 2350 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bon.tmc.edu
Center project Information
Center project name: TUNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db xref="taxon:10116"
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33822. .85574
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6668. .7475
/note="clone_boundary
clone_end:T7
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38358. .39527
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19978. .221353
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353568. .253667
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67950. .69005
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78781. .81213
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83722. .83821
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83822
253568
253668
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Db 1		Job time : 8485 secs
Qy Db 1	61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAACCACCTCAGCCCCCACCAAGCCGC 120 	
، ي	121 CGCACCCGTAGACCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC 180	
oy B	181 ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTCTGGCGACCC 240	
b cy	241 TGGGTGTGGGAGTGCTGCCGTCTTCTGCTTCCGCCGCTGCCGGATTGCCTCCAG 300	
D G	301 CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCCTGCCTGTGTACTGAGGACTCCACTGAG 360	
oy Db	361 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATGT 420	
Oy Db	421 GCACCCCCCAGCGGCGGATGGCCAGCGGCTCCAAGTCAATGGGCAGCAGCTTCAGC 480	
Qy Db	481 TACCCGGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA 540	
ôy Db	541 GCCCCTGATGCGGACTCCTGCTGCAAGGAGCCCTGGCGATCCCCCACCCA	
oy Db	601 AGCCTGCCCAGCACTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT 660	
oy Bb	661 GAGTCGGACCTGGACCTGCCGGAGATGGCCTCCATGTCGAGCCGAGAAATTGAT 720	
Qy Db	721 GIGCICATCTICAAGAAGCIGACAGAGCIGITCAGCGTACACCAGAICGATGAGCIGGC 780 	
Qy Db	781 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 840	
r A	841 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGCCGCCTGGTACGCGGC 900	
1 Bb Q	901 ATCATTGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA 960 	
oy Db	961 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGC 1020	
Oy Db	1021 TCAGGTCTCAGCCAGGATG 1039 	
Search o	completed: March 11, 2006, 22:21:20	

Aas42190 Genomic s Aax54724 Human GM-Aaa34171 Human ade Aaf20293 Human GM-

Ach7772 Human gen Adq85607 Human tum

Ab25597 Human GMAb25597 Human ade
Ab296538 Human now
Ab296538 Human now
Ab25437 Human ade
Ab25437 Human ade
Ab25437 Human ade
Ab25431 Human ade
Ab297131 Human enc
Ab29713 Human enc
Ad76889 Human cys
Ad76889 Human cys
Ad7868798 Human now
Ad888798 Human now
Ad831523 Human cDN
Ab21628 Human cDN
Ab21638 Human pol
Adx31683 Plant ful
Adx31689 Plant ful
Adx31689 Plant ful
Adx31689 Plant ful
Adx31689 Plant ful

us-09-989-890-105.rng

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comprising: a sequence encoding a sequence comprising 11-1518 amino acids is a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w isolated nucleic acid molecule, useful for treating breast cancer,
a diagnosing or monitoring the presence of metastases of breast cancer
a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer; breast cancer; breast specific; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                      Breast specific related polynucleotide SEQ ID No 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pluta J,
                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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AAX55274
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ADR89879
AACC59893
AACS28798
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ACA56890
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ADR46880
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                                                                          AB295987
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Abt13389 Breast sp
Aaf64421 Novel hum
Aaf66376 Novel hum
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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human; nucleic acid-associated protein; NAAP; cytostatic; antiarteriosclerotic; anti-HIV; antiallargic; cerebroprotective; antiparkinsonian; anticonvulsant; nootropic; neuroprotective; antiparkinsonian; ophthalmological; thyromimetic; antiarthritic; hepatotropic; antibacterial; virucide; protozoacide; antiparasitic; fungicide; gene therapy; cell proliferative disease; cancer; atherosclerosis; hepatitis; neurological disorder; Parkinson's disease; Alzheimer's disease; stroke; epilepsy; developmental disorder; renal tubular acidosis; anaemia; glaucoma; hypothyroidism;
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of the invention can be used to treat disorders by gene therapy. This polynucleotide represents a breast specific related sequence of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes human nucleic acid-associated proteins designated NAAP-1 to NAAP-57. The human NAAPs have cytostatic, antiatreriosclerotic, antiathly, antiallergic, cerebroprotective, antiparkinsonian, anticonvulsant, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, thyromimetic, antiarthritic, antiathritic, antiaflammatory, ophthalmological, thyromimetic, antiarthritic, hepatorropic, antibacterial, virucide, protocoacide, antiparasitic and ungicide activities, and can be used in diagnosing, treating and proynucleotide sequences can be used in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of NAAP, such as cell proliferative diseases (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (e.g. developmental disorders (renal tubular acidosis, anaemia, glaucoma, hypothyroidism), autoimmune/inflammatory disorders (A.BDS, allergies, atopic dermatitis, arthritis, and infections (e.g. bacterial, viral), attoimmune/inflammatory disorders (e.g. bacterial, viral)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human nucleic acid-associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,
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Elliott VS, Emerling BM, Forsythe IJ, Gorvad AE, Griffin JA;
Kable AE, Khare K, Lal PG, Lee EA, Lee SY, Li JX, Marquis JP;
Ramkumar J, Richardson TW, Sprague WW, Swarnakar A, Tang YT;
Chawla NK, Warren BA, Yue H;
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autoimmune disorder; inflammatory disorder; AIDS; allergy; atopic dermatitis; arthritis; infection; gene; ss.
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11-JAN-2002; 2002US-0347633P.
25-JAN-2002; 2002US-0351749P.
22-FBB-2002; 2002US-0359498P.
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                                                                                                                                                       TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG
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                                                                                                                                                                                                                                                                                                                                     Human; 88; gene; pharmaceutical; diagnostic; gene therapy;
tissue regeneration; cell regeneration; membrane protein;
signal transduction-related protein; transcription-related protein;
osteoporosis; neurological disease; cancer; tumour.
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ai K, Irie F
Masuho Y;
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/*tag= a // tag= a // product= "Clone KIDNE20157100 protein"
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Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, M
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide or its partial peptide, immunologically assaying the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contexting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polypucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe or context and an antisense polynucleotide. The oligonucleotide or proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related context and performed or genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell cregeneration. Membrane proteins, disease-related proteins and genes concern the activity or expression of the encoded protein and genes concern the activity or expression of the encoded protein to treat diseases. The sequence concerned is a cDNA of the invention. Note: Some of the sequence the based on sequence information supplied by the European Patent Office.
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Claim 1; Page; 222pp; English
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The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosting, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                 Human; gene therapy, vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal; gene; ss.
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invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence encodes a lung specific nucleic acid
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1249 1189 1573 1453 1513 1309 1369 1429 1489 1549 1609 1669 1069 1393 1633 1693 1753 1813 1873 1933 vulnerary; CNS-gen.; gene therapy; diagnostic; forensic; mapping; bly purification; protein purification; osteoarthritis; antiarthritic; osteogathic; musculoskeletal disease; osteoarthritis; endocrine disease; periodontal disease; antiinflammatory; mouth disease; burns; injury; peripheral neuropathy; Alzheimers disease; neuroprotective; nootropic; degeneration; parkinsons disease; antiparkinsonian; neurological disease; cerebrovascular ischemia; cerebroprotective; vasotropic; cardiovascular disease; autoimmune disease; immunosuppressive; immune disease; viral infection; virucide; infection; cancer; 1454 ACTGCTAACCCTGCCAGGCCCAGCTGCCACTTTCTGGGAGAAGCATGGCCTACAG 1574 chdchcchchcchladenagartchgaccargracatrcacagacar 1754 AGTGAACCCTGACTCCATCCCCCTATTGCCCCCTAACCAATCATGCAAACTTCTCCCCTC 1214 Additicalicalicadericadericaciócical de la Additicació de la Additical de la Additical de la Additical de la Additicació de la Additicación d 1274 CCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGGACGA CTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCC CTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGTACCCAGCAAGCC 1130 ATGACTCATCCTTCCAGGGCACCGACACAGACTCGTCGGGGGGCACCCTTGCTCCAGGTGT 1190 ACTGCTAACCCCTGCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCCTACAG 1250 AATGAAGAGGGGACCAGGAACCCCTGTGGGAGAGACTTAGACCTGAAGCAGTGCCCACT 1514 AATGAAGAGGGGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACT CTGGCTCCTCCTGCCTTGGCTGACTTCCTGGACCATGTGCATTTCACTGGGCCATG GCTCATGGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGG 1694 GCTCATGGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGG 1490 AGTGAACCCTGACTCCCATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTC CCTGGGGTAATTCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATTGGGGGTGGG CAGGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTAT 1874 CAGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTAT CCATGGTGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGA 1670 CTTAACATGACCACAGTTTGTAAGTACCTCGGCCGCGACCACGC 1713 CTTAACATGACCACAGTTTGTAAGTACCTCGCTCGCGACCACGC Novel human polynucleotide SEQ ID NO 239

cytostatic; neoplasm; gene;

180

CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC

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The invention describes a new isolated polymuclectide (I) encoding a polypeptide with biological activity comprising: a nuclectide sequence of ESD ID NOS: 1-567 (fully defined); a nuclectide sequence that hybridizes to the sequence of (i) under stringent hybridization conditions; or a nuclectide sequence (ii) under stringent hybridization conditions; or a nuclectide sequence having greater than 99% sequence identity with the sequence of (i), a host cell genetically engineered to comprise (I) operatively, associated with a regulatory sequence that modulates expression of the polymuclectide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide of is: a polypeptide encoded by (I); or a polypeptide encoded by a composition comprising the polypeptide of (SEQ ID NOS: 1-567) a composition comprising the polypeptide of (3); a method of carrier; an antibody directed against the polypeptide of (3); a method of for identifying a compound that binds to the collection of polymuclectide of (3); and a collection of polymuclectides, where the collection comprising any of the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological activity, which comprises any of the amino acid sequence of SEQ ID NOS: 1-567 encoding a polymuclectide comprising any of the sequences of SEQ ID NOS: 1-567 encoding a polymuclectide with biological activity, which comprises any of the amino acid sequences of SEQ ID NOS: 1-567 encoding a polymuclectic comprising or activity, which comprises any of the amino acid sequence of SEQ ID NOS: 1-567 encoding a polymuclectide collication. The sequences and methods are useful in disaposticic, forensic, and gene sequences and products dependent on DNA and amino acid sequences. The composition and methods are useful for tradition a dispense or date and products dependent on DNA and amino acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composition and method are useful for treating a disease or disorder, e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and peripheral disease, Alzheimer's disease, Parkinson's disease, stroke, autoimmune disorders, viral infection, or cancer. This sequence encodes a novel polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAACGAGCGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CGG-CAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCCAACAAGCCGC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g. osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral
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Goodrich R, Chen R;
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Pred. No. 7.1e-196;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     , Ren F,
Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 239; 500pp; English.
                                                                                                                                                                                                                                                                                                                     Zhang J,
Zhao Q, 1
                                                                                                                                                                                                                                                                                                                                                                  Wehrman T, Weng G, Boyle B;
                                                                                                                                                                                 11-MAR-2004; 2004WO-US007412
                                                                                                                                                                                                                              14-MAR-2003; 2003US-00389559
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Best Local Similarity 99.7%;
Matches 785; Conservative
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Asundi V,
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Xue A, A
                                                                                                                                                                                                                                                                        (NUVE-) NUVELO INC
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                                                                                       WO2005049806-A2
                                          Homo sapiens.
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Ghosh M,
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            120 CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCATGGGCCAGAGAGCATTACCTTC
                                              240 TGGGTGTGGGGGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG
                                                                                                                                              CGCTGTGGGAGCCTGTGCGGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG
                                                                                                                                                              CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG
                                                                                                                                                                                                                                                          420 GCACCCCCCAGCCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC
                                                                                                                                                                                                                                                                                                                                          <u> AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT</u>
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                                                           180 ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCCACCTGCTGCTGCTTGGCGACCC
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                                                                                                                                                                                             GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT
                                                                                                                                                                                                                                             GCACCCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC
                                                                                                                                                                                                                                                                                           TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA
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(first entry)

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Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; 88.
                                                Human gene expression product cDNA sequence SEQ ID NO:4887
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human genes and their expressed in different cell
                                                                                                                                                                                                                                                                                                                                                                                      Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-494092/41.
                       12-OCT-1999
                                                                                                                     Homo sapiens
                                                                                                                                           WO9938972-A2
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03-APR-1998;
21-OCT-1998;
28-OCT-1998;
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31-MAR-1998
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  AAZ17414;
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                                                                                                                                                                                                                                                                                                                            (HXSE-)
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Matches
 The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is
                                                                                                                                                                                                                                                                                         89 ATGATAAACCACCTCAGCCCCCACCAAGCCGCCGCACCGTAGACCAGGACCCCAAGGACC 148
                                                                                                                                                                                                                                                                                                                                       CTGGCCACCATGGGCCAGAGGATTACCTTCATCTTGGCTCTGCTGAGCCGGCCCTTG 208
                                                                                                                                                                                                                                                                                                                                                     CTGGCCACCATGGGCCAGAGAGCATTACCTTCATCTCTGGCCTCTGAGCCGGCCCTTG 120
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                                                                              New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therapy.
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                                                                                                                                                                                                                                                                                                      AGGAGCCACTGCCCGATCCCCATGCGACACAGCCTGCCCAGCACCTTTGCCAGTA
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                       Cafferkey
                                                                                                                                                                                                                                        DB 6; Length 654;
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                                                                                                                                                                                                                                                                  Indels
                        Karra K,
                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                       35.5%; Score 607.6; DB 6; 96.6%; Pred. No. 7.8e-154; tive 0; Mismatches 19;
                        Recipon H,
                                                                                                                                                                                           coding sequence of the invention
                                                                                                                               Claim 1; Page 248; 367pp; English
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                                                                                                                                                                                                                                                    Best Local Similarity 96.6
Matches 632; Conservative
                      S, Macina RA,
Liu C;
DIADEXUS INC
                                                          WPI; 2002-657582/70.
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expression products which are differentially types.

Labat I;

J, Innis MA, Garcia PD, Sudduth-Klinger Randazzo F, Kennedy GC, Pot D, Kaseam A, Crkvenjakov R, Dickson M, Drmanac S, Lab Garcia V, Jones WL, Stache-Crain B;

LT, Escobedo I C, Giese K, 3, Drmanac R, Escobedo

CHIRON CORP.

HYSEQ INC

98US-0072910P. 98US-0075954P. 98US-0080114P. 98US-008066EP. 98US-0105234P. 98US-0105234P.

99WO-US001619

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The present invention describes a library of human polynucleotides

comprising the sequences given in AAZ12532 to AAZ1779. Also described is

a method of detecting differentially expressed genes correlated with the

cancerous state of a mammalian cell, comprising detecting at least one

differentially expressed gene product in a test sample from a cell

suspected of being cancerous, where the gene product is encoded by one of

the 5148 polynucleotide sequences given in AAZ12532 to AAZ1779. The

polynucleotides can be used as a source of primers and probes, which can

be used for a variety of purpose, e.g. detection of expression levels,

mapping, tissue typing or profiling, forensice, genetic analysis and

detection of polymorphisms. Polypeptides encoded by the polynucleotides

can be used for raising antibodies for experimental, diagnostic and

cheropetic purposes. The polynucleotides may also be used to construct

arrays for diagnostics (which may be used to determine function of an

encoded protein); and to detect differences in expression levels between

two cells (e.g. to identify abnormal or diseased tissue in a human, to

identify a genetic predisposition or susceptibility to a disease such as

cancer). The polynucleotides of the invention are especially used in the

diagnosis, prognosis and management of colorectal cancer, became to the construction and management of colorectal cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 728 BP; 145 A; 190 C; 178 G; 150 T; 0 U; 65 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
Claim 1; Page 2323-2324; 2479pp; English.
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Best Local Similarity
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AAZ17414 standard; cDNA; 728

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cancer and non-cancerous diseases of the lung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer;
           151 GGGCCGGCTGGTACGCTGGATCATTCNCATTAGTNCCCGAAAGAGCCGTGCTTGGCNACA
                                                       211 GA-CTCCGAGGGTCGTTCAACT-NGGCTGCTGTCCCAAACGCTGCTGACCCTGACCCTGACACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 CTGGCTCCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATG 1369
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                                            The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-1421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, invention are used for identifying ung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence encodes a lung specific nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.5%; Score 385; DB 6; Length 38 Best Local Similarity 100.0%; Pred. No. 1.2e-93; Matches 385; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 385 BP; 80 A; 122 C; 93 G; 90 T; 0 U; 0 Other;
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Claim 1; Page 204-205; 389pp; English.
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comprising: a sequence encoding a sequence comprising 11.1518 amino acids a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 190-8144 nt sequence. The polympeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polymucleotides of the invention can be used to treat disorders by gene therapy. This polymucleotide represents a breast specific related sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1436 GGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAA 1495
                                                                                                                                                                                                      New isolated nucleic acid molecule, useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 CCCTGACTCCATCCCCCTATTGCCACCATACATCATCATGCAAACTTCTCCCCTGGG
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                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated nucleic acid molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 386 BP; 81 A; 121 C; 94 G; 90 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 380.2; DB 8;
Pred. No. 2.3e-92;
n. Mismatches 3;
                                                                                                                     Pluta J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polynucleotide, SEQ ID NO: 177.
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                                                                                                                       Recipon H,
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                                                                                                                                                                                                                                                                                     Claim 1; Page 250; 377pp; English
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21-NOV-2001; 2001WO-US043815
                                      22-NOV-2000; 2000US-0252509P
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99.2%;
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Best Local Similarity 99.2
Matches 382; Conservative
                                                                                                                       Macina RA,
                                                                              (DIAD-) DIADEXUS INC
                                                                                                                                                             WPI; 2003-018927/01.
                                                                                                                                                                                                                                                 in a patient.
                                                                                                                   Salceda S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGGGGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 GGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer; metastatic; breast cancer; breast specific; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1196 AACCCCTGCCAGGCCCAGCTGCCACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAA
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                                                         Cafferkey R;
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                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 386 BP; 81 A; 121 C; 94 G; 90 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breast specific related polynucleotide SEQ ID No 104
                                                         Karra K,
                                                                                                                                                                                                                                                                                                                                                                                                                           Match 22.2%; Score 380.2; DB 6; Local Similarity 99.2%; Pred. No. 2.3e-92; es 382; Conservative 0; Mismatches 3;
                                                         Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1556 GTAATTCAACAGTTAAAAGAAGCTT 1580
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                                                                                                                                                                                                                                                                                                                                              a coding sequence of the invention
                                                                                                                                                                                                                                            Claim 1; Page 248; 367pp; English
                                                         Hu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABT13389 standard; DNA; 386
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                                                       Salceda S, Macina RA,
Sun Y, Liu C;
                 DIADEXUS INC
                                                                                                                   WPI; 2002-657582/70.
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ATGCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG 139
321 GGAGCTCCAGGGTACCCAGCAAGCCATGACTCATNCTTTCAGGGGCACCGACACAGACTC 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGCCCCGCCCTGGACACCCCCCGCCCACCATCTGGGCCTTCCACGCTTGGGACCGTGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; ss.
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or Kita D, Garcia V, Jones LW, Strache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 427;
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20.3%; Score 347; DB 5; Length 42
Best Local Similarity 99.7%; Pred. No. 2.4e-83;
Matches 347; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escobedo J, Innis MA, Garcia PD, inhard C, Randazzo F, Kennedy GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polynucleotide, SEQ ID NO: 2132.
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                                                                                                                                                                                                                                                                                                                AAF66376 standard; cDNA; 427 BP
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                                                                       1164 GTCGGGGCACC 1175
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dysplasia and hyperplasia
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02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            805 CTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTG 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klinger J;
Pot D, Lam
Labat I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garcia PD, F
Kennedy GC, F
, Dickson M,
   breast cancer; lung cancer; cancer detection; ss.
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Reinhard C, Randazzo F, Kennedy G
Crkenjakov R, Drmanac S, Dickson
z D, Kita D, Garcia V, Jones LW,
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98.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-091805/10.
                                                                                                                                           WO200102568-A2
                                                                                                                                                                                                                                                                                                                                                02-JUL-1999;
02-JUL-1999;
                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams LT,
                                                                                                                                                                                                               11-JAN-2001.
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Огтапас R,
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Lamson G;

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CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC 120
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                                                                                          The present invention describes a library of human polynucleotides comprising the sequences given in AA212532 to AA217779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
                                                           CGCACCCGTAGACCAGGACCCCTGGCCCACCATGGGCCAGAGAGCATTACCTTC 259
                                                                                                                                    TGGGTGTGGGAGTGGTGCCTCCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG 379
                                                                                                                         TGGGTGTGGGGAGTGGTGCCGCGGCTGCTTCTGCTTCCGCCGCCTGCCGGGATTGCCTCCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human genes and their expression products which are differentially expressed in different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
Jises K, Randazzo F, Kennedy GC, Pot D, Kassam A;
nanac R, Cikvenjakov R, Dickson M, Drmanac S, Labat I;
Kita D, Garcia V, Jones WL, Stache-Crain B;
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                                          CGCACCCGTAGACCCCAAGGACCCTGGCCACCTTGGGCCAGAGAGCATTACCTTC
                                                                                                                                                                                                                                                                                                                      Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                  CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCTTGCCTGTCTACTGAG 348
                                                                                                                                                                            CGCTGTGGAGCCTGTGTGGGGGGGGCCCCTGCCTGTCTAAA 427
                                                                                                                                                                                                                                                                                                   Human gene expression product cDNA sequence SEQ ID NO:861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 860; 2479pp; English.
                                                                                                                                                                                                                                        BP.
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98US-0075954P.
98US-0080114P.
98US-0080515P.
98US-0080666P.
                                                                                                                                                                                                                                       AAZ13392 standard; cDNA; 300
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98US-0105877P.
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24-FEB-1998;
31-MAR-1998;
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28-0CT-1998;
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03-APR-1998
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polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypetides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAGACCATGGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGAGATCTCCCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 300 BP; 63 A; 96 C; 90 G; 51 T; 0 U; 0 Other;
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Matches 300; Conservative
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03-APR-1998;
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This invention describes novel isolated human polymucleotides obtained by screening for differential expression in colon cancer, breast cancer and lung cancer call lines. The polymucleotides of the invention are represented in AAX98275-X991B and encode polypeptides of protein families selected from 4 transmembrane segments integral membrane proteins, 7 transmembrane receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of transcription factors, G-protein alpha subunit, phorbolesters or diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, cranscription factors, trypsin, wut family of developmental signalling proteins and WM/rsp5/WWP domain containing proteins. The crepat, basic region plus leucine zipper transcription factors, crepat, basic region in the plus leucine zipper transcription factors, credition in the plus leucine zipper transcription factors, creditions in the products for use as therapeutic polymucleotides can be used to develop products for use as therapeutic agents and in forensics, genetic analysis, mapping and diagnostic applications. In particular, the product can be used for treating e.g. cervical cancers, melanomas, colorectal adenocarcinomas, wilm's tumour, sarcomas, retinoblastoma, myosarcomas, lung carcinomas, leukemia, and lymphomas such as histiocytic lawkemia, and management of cancers. They can be used for traeting e.g. cervical myelogenous leukemia, and lymphomas such as histiocytic lawkemia, and management of cancers, fibrous dysplasia, ongential aleukemia, and lymphomas such as histiocytic lawkemia, and hyperplasias, e.g. endom
                                                                                                                                                                             Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
Alsee K, Randazzo F, Kennedy GC, Pot D, Kassam A,
Ananac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Kita D, Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                           New isolated human polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 326; 591pp; English.
98US-0105234P.
98US-0105877P.
98US-00217471.
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Drmanac R,
                                                                                                         CORP.
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                                                                                                    (CHIR ) CHIRON COR
(HYSE-) HYSEQ INC.
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Reinhard C,
                            27-OCT-1998;
21-DEC-1998;
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Sequence 300 BP; 68 A; 90 C; 86 G; 56 T; 0 U; 0 Other;

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March 11, 2006, 19:52:41 ; Search time 6305 Seconds (without alignments) 12711.542 Million cell updates/sec
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SUMMARIES	CR749558 DO045548	DQ045549	AK007551 BM460277	AK051860	CN289134	BQ691555	BY707606	BE741035	BE901537	BM823479	BP315176	BI694617	BP331524	AA573775	AA316608	CK478920	BF135747	AI925416	BI411303	BI653517
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Score	1451.2	1145	951.8	791	731.4	687	9.629	669.4	647	622	577.8	576.2	540.2	526.6	510	496.4	489.2	480.2	476	470.6
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1 (bases 1 to 1197)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B..
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Pan troglodytes FLJ34633 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. DQ045549 GI:66896764
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Pan troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
1 (bases) to 1181)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.
Nielsen, R., Bustamante, C., Tanenbaum, D.M., Civello, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
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                                                                                                                    GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC
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Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B. Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B. Whelse,T.J., Sinnsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans
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100.0%; Pred. No. 1.1e-296;
tive 0; Mismatches 0;
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/ Organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                     A Scan for Positively Selected Gen
Chimpanzees
(er) PLoS Biol. 3 (6), E170 (2005)
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/gene="FLJ34633"
/locus_tag="HC11301"
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Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs

Nature 420, 563-573 (2002)
6 (bases 1 to 1657)
Adachi,J., Alzava,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
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                                                                                                                                            ATCATTCGCATTAGTACCCGAAAGAGCCGTCGCTCGCCCACAGACCTCGGAGGGTCGTTCA
                                                              TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCCAGGAGACGACTGCAGATGCC
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Mus musculus 10 day old male pancreas CDNA, RIKEN Full-Length enriched library, clone:181001916 product:SIMILAR TO TATA BOX BINDING PROTEIN (TPD) -ASSOCIATED FACTOR, RNA POLYMERASE II, CI. 130KD homolog [Mus musculus], full insert sequence.
                                         ACTOGGGCTGCTGCCCCAACCGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGCC
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Nature 409, 685-690 (2001)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
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Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon start=1
/protein id="BAC25177.1"
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PLABPPPTRBLPSTFTNSPRGSTSFSFSFSTDLDPEWGSGSMSSRIDVLFKKTT
BLFSVHQIDBLAAKTSDTVFLEKTSKISDL.1SSITQDYHLDBQDAEGRLVRGTIRIST
RKSRSRPQTSEGRSARSTAPPAAAPDSGHETWLGSGLSQDELTVQISQSTTADAIARKL
                                                                                                                                                                                                                                                                                             Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.jp/) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG
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Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kabikwa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M. Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K. Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C. Saito,H., Saato,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Suito,H., Saito,R., Shinata,X., Shinata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Tejima,Y., Toya,T., Yamamura,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="FANTOM_DB:1810019J16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pancreas"
/clone_lib="RIKEN full-length
/dev_stage="10 day old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="1810019J16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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Best Local Similarity 82.2
Matches 1173; Conservative
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Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230011M17 product:hypothetical protein, full insert sequence.

AKO51860
AKO51860.1 GI:26342255
HTC: CAP trapper.
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                  181 ACATCAGACCTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATC
ACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGCATCATT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/mol type="mRNA"
/db Xref="taxon:9606"
/clone="IMAGE:5502726"
/tissue type="retinoblastoma"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                         975 bp mRNA linear EST 05-FEB-2002
AGENCOURT 6420313 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502726
5'', mRNA Sequence.
                                1244 CCTACTGGCCCAGCAGTCACGGCTCTCCTGGAAGAAGCATAGCCAGC----GGAGGAGA 1299
                                                                                     GGGACCAGGAACCC---CTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTC 1316
                                                                                                                         1300 GGAACCAGGACCTCTGTGTGGGGCCGCCTCTGAGCCGAGAAGCAGTGACCTCTCTGGCTT 1359
    CCTGCCAGGCCCAGCTGCCACACCCTTTCTGGAAAAGCATGGCCTACAGAATGAAGAGG 1259
                                                                                                                                                                                                        1360 CTGCTTTTGTTGAATCC----CCTTAGACCACATACATTTCACAGGGCCATGGTGCCCA 1414
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I (bases 1 to 975)

S NIH-MGC http://mgc.nci.nih.gov/.

Inth-MGC http://mgc.nci.nih.gov/.

Inth-MGC http://mgc.nci.nih.gov/.

Inth-MGC http://mgc.nci.nih.gov/.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATC

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at:

http://image.lnl.gov

Plate: LLAM12141 row: f column: 07

High quality sequence stop: 659.

Location/qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

IL Nature 420, 563-573 (2002)

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E Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Kasuka, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakaukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Okazaki, V., Saito, R., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takaku, A., Takahashi, F., Takaku-Akahira, S., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Direct Submission
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                genes
                                                                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new g
Genome Res. 10 (10), 1617-1630 (2000)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="RaNTOM DB:D230011M17"
/db_xref="taxon:<u>1</u>0090"
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/Leimslation="MLVLSLWPSRRLGGARSGLGGTPLCSLAQAASADPSMGSPADKQ
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CCSQAPAGRSQBEVRDKLLG"
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Pred. No. 3.8e-192;
0; Mismatches 145; Indels
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Matches 891; Conservative
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AGENCOURT 8341018 NIH_MGC_110 homo sapiens cDNA clone IMAGE:6249453 5', mRNA Sequence. BQ691555.1 GI:21816871 EST.
                                                                                                                                                          309 AGGAGCCACTGGCCCGATCCCCCACCCATGCGACAGCCTGCCCAGCACCTTTGCCAGTA 368
                                                                                                                                                                                                                                               685
                               249 TCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCAGCCCCTGATGCGGACTCCTGCTGCA 308
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                                                                                                                                                                                                                                                                           369 GTCCTCGTGGCTCCCGAGGAGTACTATTCTTTCCATGAGTCGGACCTGGACCTGCCGGAGA 428
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                          566 AGGAGCCACTGGCCGATCCCCCACCCATGCGACACAGCCTGCCCAGCACCTTTGCCAGTA
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1 (bases 1 to 917)

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Tissue procurement: ACC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arged by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can bettp://image.llnl.gov
ttp://image.llnl.gov
plate: LLCM3390 row: o column: 22
High quality sequence stop: 535.
High quality sequence stop: 535.
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from MNGO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
393 GCCGCTCTACTGCCC---CTGCTGCTGCCCCCGACAGTGGCCATGAGACCATGCTGGGC 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., XW. C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.M. Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="t=axon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 CTICTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCGCTGTGGAGCCTGTGTGCGGGGGATG 68
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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17000599935935 GRN_PREHEP Homo sapiens CDNA 5', mRNA sequence
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Fax: 650 473 760
Email: rbrandenberger@geron.com
Insert Length: 753 Std Error: 0.00.
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Pred. No. 7.4e-177;
0; Mismatches 1;
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Regenerative Medicine
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1 (bases 1 to 753)
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Mus musculus (house mouse)

Mus musculus

Bukaryota, Mesazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota, Mesazoa; Chordata; Buarchontoglires; Glires; Rodentia;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Murinae; Mus.

'L. a. 1 to 1009)

BY707606 BY707606.1

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

us-09-989-890-105.rst

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/clone lib="NIH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1, cDNA made by oligo-dr priming.
Site_2: according to the stress of sites using the following S' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                             Gaps
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;
                                                                                                                                                                                                                40.1%; Score 687; DB 5; Length 917; 98.3%; Pred. No. 2.1e-165; ive 0; Mismatches 10; Indels
                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.3
Matches 715; Conservative
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BY707606 BIKEN full-length enriched, 10 day old male pancreas Mus musculus cDNA clone 1810019016 5', mRNA sequence.

LOCUS RESULT 9 BY707606

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Scillogopathi, murbicaes; murines; mus.

Scillogopathi, murbicaes; murines; mus.

Scillogopathi, murbicaes; murines; mus.

Nikaido, T., Osato, N., Saito, R., Suzuki, H.; Yamanakai.

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Mateuda, H.,

Batalov, S., Beisel, K., Frazer, K.S., Dalla, E., Dragani, T.A.,

Fletcher, C.P., Forrest, M., Frazer, K.S., Dalla, E., Dragani, T.A.,

Fletcher, C.P., Godzins, A., Gaugh, J., Grimmond, S.,

Gariboldi, M., Gissi, C., Godzin, A., Gaugh, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kurochkin, I.V., Lee, Y., Lehard, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lehard, B.L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pescole, G.,

Petrovsky, N., Pillai, R., Pontius, Ju., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pescole, G.,

Baraid, R., Schneider, C., Semple, C.A., Setou, M., Shinada, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, M.,

Verardo, R., Walming, L.G., Wynshaw, Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatcu, N., Hirozane-Kishikawa, T., Kawai, K., Kawai, J., Aizawa, K.,

Rakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., India, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Rogers, J., Birney, E. an
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Fax: 81-45-503-922  
Exa: 81-45-503-9216  
Email: genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/ Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Ruda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sanc, H., Sasaki, D., Sato, K., Shibata, K., Shizaki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramateu, M., and Hayashizaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp) for
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/tissue type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 9"
/note="Organ: ovary; organ: ovary; o
                                                                                                                                                                                                                                                                                                                                                                               BE741035 1015 bp mRNA linear EST 15-SEP-2000 601594018F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947861 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             824 CAAGTGCACATCGGACACCGTGCTCCTGGAGAAGACCAGCAAGATCTCAGACCTGATCAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM810 row: d column: 06
High quality sequence stop: 752.
Location/Qualifiers
1. 1015
                                                            840 CAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGG
                                                                                          GCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCCAAGCCGCCG
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1 (bases 1 to 1015)

NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                              941 garcarcciarradrarcecaaaacrecrececeaeaeaereceaeaeaere
                                                                                                                                                                           18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3947861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE741035.1 GI:10155027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 IGAATCGGACCTGGACCTGCCTGAGATGGGCAGTGCCTCCATGTCGAGCCGGGAGATCGA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     764 CGTGCTTATTTTCAAGAAGCTGACAGAGCTGTTCAGCGTGCACCAGATTGACGAGCTGGC 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                               /tissue_type="pancreas"
/dev_stage="10 day old"
/clone_lib="RIKEN full-length enriched, 10 day old male
pancreas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 ATGCCCAGGCCGGACAGCCCCGCCCATCATGGGCCTCCACGCTTGGGGCCCTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 AGGCCATCAGAGTTATGCCTGGAAACGAACGATGAGGCGCTCCCAGCCCCCACCGGGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCACCAGGAGGCCAGACCCTAAGGACCCTGGCCACCACGGGCCAGGAGGAGTATCACCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 679.6; DB 5;
Pred. No. 1.7e-163;
                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                        db_xref="taxon:10090"
clone="1810019J16"
                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  39.7%;
84.0%;
                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 803; Conservative
                                                               1. .1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464
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cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.B. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM842 row: g column: 05
High quality sequence stop: 668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACCACCTCAGCCCCCACCAAGCCGCCGCACCCGTAGACCAGACCCAAAGGACCCTGG-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 ATGGAGTGCCCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCGGGATGGCCAGCGGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 AACCACCTCAGCCCCCACCAAGCCGCCCCCCCTAGACCCAGACCCCAAGGACCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCATGGGCCAGAGCATTACCTTCATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCATGGGCCAGAGAGCATTACCTTCATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 37.8%; Score 647; DB 2; Length 966; al Similarity 93.9%; Pred. No. 4.2e-155; 750; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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601677420F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960220 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                              ACCCCCAGCCGGCGGATGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCAGCTTCAGCTA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  542
                                                                                                                                                        CTGTGGAGCCTGTGTGTGTGGGGGATGCAGCCCCTGTCTACTGAGGATTCCACTGAGGG 305
                                                                                                                                                                                                                                  422
                                                                                                                                                                                                                                                                GACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCCAGCCCTGATGGTGC 365
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1 (Bases 1 to 966)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                              GGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCCTGCCGGGATTGCCTCCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCGATGITAAGCTCAAAGGCATCCTGTGTATCCCTACCGAGGGCCACCTCCCCAGC
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ATCTCCCAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCA 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1294 TGAAGCAGTGCCCACTCTGGCTCCTCCTGGCTTGGGTTGGGTTCCTGGACCATGTGC 1353
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1 (bases 1 to 582)

2 suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Makai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

Block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                 GACAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGAGTGCAG
                        61 GATGCTGAGGGCCGCCTGGTACGGGGCATCATTAGTACCCGAAAGAGCCGTGCT
                                                                                                            CGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCT
                                                                                                                                                                        GACAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAG
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GATGCTGAGGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCCCGAAAGAGCCGTGCT
                                                                                   CGCCCACAGACCTCGGGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCT
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: guzuki@ins.u-tokyo.ac.jp.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OFR07979"
/tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1414 GGGCCCCTTCCTTCTGCTCAT 1435
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/cell_line="SNU-16"
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/clone_lib="S22SNU16nl"
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Site_2: NotI; The $22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F. Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."
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K-EST0094733 S22SNU16n1 Homo sapiens CDNA clone S22SNU16n1-102-H01
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
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                      AGCGTACACCAGA---TCGATGAGCTGGCCAAGTGCACATCAGACACTGTGTTCCTGGAG 810
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                                                                                                                                    814 ACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAG 873
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                         AAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAG
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Vuseong-gu, Daejeon 305-333, South Korea
Fax: +82-42-860-4470
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/organism="Homo sapiens"
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Plate: 102 row: H column: 01
High quality sequence stop: 622.
Location/Qualifiers
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BM823479.1 GI:19179892
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60334938F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5375384 5',
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
              gland OCUB-F"
                                                                                                                            AACATGGGCAGCAGCATCAGCTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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                                                              Length 582;
               mammary
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                                                            Score 577.8; DB 3;
Pred. No. 2.5e-137;
0; Mismatches 2;
/cell_line="OCUB-F"
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/db_xref="haxon:10000"
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/dev_stage="5 months"
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCWV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11955 row: 1 column: 09 Plate: LLAM11955 row: 1 For thigh quality sequence stop: 796.
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Pred. No. 6.8e-137;
0; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                  musculus"
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/organism="Mus
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us-09-989-890-105.rst

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              GGCTCAGGTCTCAGCCA--GGATGAGCTGACAGTGCAGATCTCCCCAGGAGACGACTGCAG 1075
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                              717 GGCTCTGGCCTCAGCCACGGACGGACTGACACTCACGATCTCCCAGGAGGACAACCGGA 776
                                                                                                                                                                                                                                                                                                                                  Hominidae, Homo.

1 (bases 1 to 583)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

Block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yazuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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Corganisms=Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="KT09506"

/tisaue_type="rectum"

/clone_lib="sugano_cDNA_library, rectum"
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                                                                        1076 ATGCCATCGCCCGGAAGCTGAGGCC 1100
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Search completed: March 11, 2006, 22:01:33 Job time : 6313 secs

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Sequence 799, App Sequence 2, Appli Sequence 1488, Ap Sequence 153, App Sequence 6029, Ap Sequence 6078, Ap Sequence 3, Appli Sequence 1, Appli Sequence 11, Appli Sequence 9140, Appli 91
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Sequence 14290, A
Sequence 14291, A
Sequence 42, Appl
Sequence 17202, A
Sequence 14, Appl
Sequence 1656, A
Sequence 1656, A
                                                                                                                                                                                                                                                                                               March 11, 2006, 19:54:43 ; Search time 324 Seconds (without alignments) 9398.034 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-016-434-1488
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US-09-489-039A-6029
US-09-489-039A-6072
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US-09-797-039-1
US-09-797-039-1
US-09-620-312D-20
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US-09-0734-030-1
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US-09-902-540-9140
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Maximum Match 100%
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seq length: 200000000
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Sequence 6144, Ap Patent No. 5221620 Sequence 112, App Sequence 27, Appl Sequence 1352, A Sequence 17572, A Sequence 1152, App Sequence 1152, Appl Sequence 1154, Appl Sequence 1166, A Sequence 1160, Appl Sequence 1160, Appl Sequence 1160, Appl Sequence 1160, Appl Sequence 1160, A Sequence

390 CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCTGCCTGTCTACTGAGGACTCCACTGAG 449

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TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG
                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09103840A;
Sequence 2, Application US/09103840A;
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, OWEN R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN;
TITLE OF INVENTION: DNA SEQUENCES;
TITLE OF INVENTION: DNA SEQUENCES;
TITLE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO
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COTHER INFORMATION: "n" bases at various
CHER INFORMATION: represent a, t, c or
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US-09-016-434-1488
Sequence 1488, Application US/09016434
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; GENERAL INFORMATION:
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Best Local Similarity 50.0%;
Matches 115; Conservative
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                                GGGACTGCTGAAGCCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT
                                                                                         510 GCACCCCCCAGCCGGCGGGATGGCCAGCACTCAAGTCAACCATGGGCAGCAGCTTCAGC
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                                                                                                                                                                                             AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT
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SOFTWARE: FastSEQ for Windows Version 3.0
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Parent No. 6444425
GENERAL INFORMATION:
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Patent No. 6759508
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Best Local Similarity 46.9%;
Matches 129; Conservative
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US-09-370-838-153
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACTER
STREET: 3174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42.2; DB 3; Length 1767;
Pred. No. 0.42;
0; Mismatches 218; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURENT APPLICATION NUMBER: US/09/016,434
FILLING DATE: HEREWITH
CLASSIFICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DALL.

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:

""T.RPHONE: (650) 855-0555
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Best Local Similarity 48.3%;
Matches 215; Conservative
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; CLONE: 9995934
US-09-016-434-1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302
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Pred. No. 0.74;
0; Mismatches 146; Indels 0
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.4.545.09
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
SARLIER APPLICATION NUMBER: US 09/285,323
SARLIER PILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
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APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21012. 475C10
CURRENT APPLICATION NUMBER: US/09/854,133
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Sequence 6072, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                        Query Match 2.4%; Score 40.8; DB 3; I
Best Local Similarity 48.6%; Pred. No. 0.76;
Matches 140; Conservative 0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR PRLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
SEQ ID NOS: 14342
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ORGANISM: Klebsiella pneumoniae
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SEQ ID NO 6072
LENGTH: 465
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US-09-489-039A-6072/c
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GENERAL INFORMATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489, 039A

CURRENT APPLICATION NUMBER: US/09/489, 039A

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29
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46.9%; Pred. No. 0.74;
tive 0; Mismatches 146; Indels
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ORGANISM: Klebsiella pneumoniae
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SEQ ID NO 6029
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Best Local Similarity 46.9
Matches 129; Conservative
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                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapien
US-09-854-133-153
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US-09-489-039A-6029
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                                                                                   LENGTH: 2109
SEQ ID NO 153
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126 CCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTCATCTC 185
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; Sequence 3, Application US/09797039
; Patent No. 6730491
; GENERAL INFORMATION:
; APPLICANT: Clandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: 10448-017001
; CURRENT APPLICATION NUMBER: US/09/797,039
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6730491
GENERAL INFORMATION
APPLICANT: Clandt, Peter J.
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 10448-017001
CURRENT APPLICATION NUMBER: US/09/797,039
CURRENT FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
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Matches 83; Conserva
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LENGTH: 1503
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US-09-797-039-3
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US-09-797-039-1
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TITLE OF INVENTION: Dolypeptides
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/99/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: P. F. L. Genes Version 1.0
SEQ ID NO 19
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2.4%; Score 40.4; DE
Best Local Similarity 53.9%; Pred. No. 1.4;
Matches 83; Conservative 0; Mismatches
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2297
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                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (154)...(1656)
NAME/KEY: misc_feature
LOCATION: (1)...(2297)
COTHER INFORMATION: n = A,T,C or G
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GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rei, Yei, yan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Mang, Jian-Rui
APPLICANT: Mang, Ding
APPLICANT: Mang, Dunrui
APPLICANT: Gohn Tillinghast
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: (206)..(1618)
US-09-620-312D-19
                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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528 TTGACTGGATCCTGGACCAGGGCTACTACTCGGA 561
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: HUMAN
                                                             RESULT 13
US-09-734-030-1
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                                                                                713 AAATTGATGTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATG 772
                                                                                                                408 AGAACGAGATAGGCATCCTCAAGATGGTGAAGCATCCCAACATCCTACAGCTGGTGGATG 467
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ch 2.4%; Score 40.4; DB 3; Length 2747;
1 Similarity 53.9%; Pred. No. 1.5;
83; Conservative 0; Mismatches 71; Indels 0
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APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: Dramac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
CURRENT APPLICATION NUMBER: US/05/620,312D
CURRENT FILING DATE: 2000-07-19
FILOR PEDICATION NUMBER: 09/552,317
PRIOR PEDICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 100-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NOS: 1105
SEQ ID NO 20
LENGTH: 2840
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                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 656962
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunqing
Wang, Dunrui
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Best Local Similarity 53.9
Matches 83; Conservative
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Wehrman, Tom
Xue, Aidong J.
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; LOCATION: (206)..(1711)
US-09-620-312D-20
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ORGANISM: Homo sapiens
                   Best Local Similarity
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US-09-620-312D-20
  Query Match
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APPLICANT:
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Sequence 1, Application US/10153921

Sequence 1, Application US/10153921

Sequence 1, Application US/10153921

Setent No. 6653116

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENITON: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENITON: THEREOF

TITLE OF INVENITON: THEREOF

FILE REPERENCE: CLO00612D1V

CURRENT APPLICATION NUMBER: US/10/153,921

CURRENT PILING DATE: 2000-05-24

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PASESEC for Windows Version 4.0

LENGTHAN 3124
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ORGANISM: HOMO SAPIEN
US-10-153-921-1
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Matches 83; Conserv
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Sequence 1. Application US/10669689
| Patent No. 6800471
| GENERAL INFORMATION:
| APPLICANT YAN, Chunhua et al. APPLICANTY YAN, Chunhua et al. TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION THEREOF CURRENT APPLICATION NUMBER: US/10/669,689 CURRENT APPLICATION NUMBER: 09/734,030 PRIOR FILLING DATE: 2003-09-25 PRIOR FILLING DATE: 2000-12-12 PRIOR FILLING DATE: 2000-12-12 PRIOR PRIOR FILLING DATE: 2000-05-30 PRIOR SEQ. ID NOS: 3 SOFTWARE: FastEEQ for Windows Version 4.0 SECTIVARE: PastEEQ for Windows Version 4.0
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                                               713 AAATTGATGTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATG 772
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  0; Gaps
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71; Indels
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0; Mismatches
83; Conservative
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ORGANISM: Homo sapiens
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US-10-669-689-1
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Book State

Search completed: March 11, 2006, 20:06:17 Job time : 329 sec8

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March 11, 2006, 20:00:16 ; Search time 1286 Seconds (without alignments) 11015.120 Million cell updates/sec
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/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USIOA_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USIOA_PUBCOMB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9793542 seqs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA_Main:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1713
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 105, App Sequence 799, App Sequence 56, Appl Sequence 117, App Sequence 124, App Sequence 5731, Ap Sequence 55, Appl Sequence 104, Appl Sequence 104, Appl Sequence 104, Appl 10096, A 17051, A 17051, A 34, Appl 34, Appl 116, App 10967, A 6792, A 6792, A 6792, A 1484, Appl 1484, Appl 1488, Appl 1489, Appl Description Sequence 1 Sequence 1 Sequence 2 Sequence 1 Sequence 3 Sequence 1 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-989-890-105
US-09-98-920-56
US-09-989-920-56
US-09-989-920-117
US-10-779-543-5731
US-09-989-920-55
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US-10-779-543-44
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US-10-029-386-10967
US-10-039-748-83-144
US-10-733-860-3497 SUMMARIES Query Match Length DB 120 2761 513 1242 2359 2370 1412 1767 Score 42.8 42.2 42.2 18 19 20 21 22 23 Result υυ υu

nce 7, Appli	7	nce 17895, Ā	nce 4195, Ap	nce 7952, Ap	nce 7951, Ap	nce 120331,	nce 153, App	nce 153, App	nce 153, App	nce 28779, A	nce 48, Appl	48,	nce 5477, Ap	nce 10204, A	nce 1003, Ap	nce 3760, Ap	nce 120327,	nce 3762, Ap	_	9	nce 71259, A
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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2389	2429	237	593	1518	1830	1696	2109	2109	2109	3267	4988	4988	13862	13862	13862	1324	1845	5592	15738	37360	9
2.5	2.5	2.5	2.5	2.5	2.5	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4
42.2	42.2	42	42	42	42	41.8	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.2	41.2	41.2	40.8	40.8	40.6
24	25	26	27	28	29	30	c 31	c 35	c 33	34	c 35	c 36	c 37	c 38	39	c 40	41	c 42	c 43	n 44	45

ALIGNMENTS

ods Relating to Breast Specific Genes and B	1; DB 3; Length 1713; 0; DB 3; Length 1713; 0; DB 0; Indels 0; Gaps 0; 1: CCTGGGCCTCCACGCTGGGAG 60 1: CCTGGGCCTCCACGCTGGGAG 60 1: CCTGGGCCTCCACGCTGGGAG 60 1: CCTGGGCCTCACGCTGGGAG 60 1: CCTGGGCCTCAGCCCCCAAGCCG 120 1: CCTGCCATGGGCCAAGCCG 120 1: CCTGCCATGGGCCAGAGCGT 180 1: CCCCCATGGGCCAGAGAGCATTACCTTC 180 1: CCCCCATGGGCCAGAGAGCATTACCTTC 180 1: CCCCCACTGCTGCTGCTCTGGGACCC 240 1: CCCCCACTGCTGCTCTGGGACCC 240 1: CCCCCACTGCTGCTCTGGGACCC 240 1: CCCCCCACTGCTGCTCTGGGACCC 240 1: CCCCCCACTGCTGCTCTGGGACCC 240 1: CCCCCCACTGCTGCTCTGGCACCC 240 1: CCCCCCACTGCTGCTCTGGGACCC 240 1: CCCCCCACTGCTGCTCTGGCACCC 240 1: CCCCCCACTGCTGCTCTCGGGACCC 240 1: CCCCCCACTGCTGCTCTCGGGACCC 240 1: CCCCCCACTGCTGCTCCTCGGGACCC 240 1: CCCCCACTGCTGCTCTCCAG 300
SULT 1 -09-989-800-105 -09-989-800-105 -09-989-800-105 -00-989-800 -00-989-800 -00-989-800 -00-989-800-105 -00-989-890 -00-99-999-900 -00-9-989-900 -00-9-989-900-105 -00-9-989-990-105 -00-9-999-990-105 -00-9-999-990-105	100.0%; Score 1713; DB 100.0%; Pred. No. 0; vative 0; Mismatches ccredacacccccccccacarcredegc GHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
RESULT 1 US-09-989-890-105 US-09-989-800-105 Sequence 105, Application Sequence 105, Application GENERAL INFORMATION: APPLICANT: Salceda, Susan: APPLICANT: Recipon, Hervapplicant Recipon, Hervapplicant; Putta, Jason APPLICANT: Pluta, Jason APPLICANT: Liu, Chenghua TITLE OF INVENTION: Compon FILE REPERENCE: DEX-0287 CURRENT APPLICATION NUMBES CURRENT APPLICATION NUMBES CURRENT FILING DATE: 2000-11 NUMBER OF SEQ ID NOS: 280 SOFTWARE: Patentin version; SEQ ID NO 105 LENGTH: 1713 TYPE: DNA GRGANISM: Homo sapien US-09-989-890-105	Query Match Similarity Best Local Similarity Andeceded Qy 1 ATGCCCGC Qy 61 CGGCCAACA Qy 61 CGGCCAACA Db 61 CGGCCAACA Oy 61 CGGCCAACA Oy 61 CGGCCAACA Oy 121 CGCACCCGT Db 121 CGCACCCGT Oy 121 CGCACCCGT Oy 181 ATCTCTGGC Oy 181 ATCTCTGGC Oy 241 TGGGTGTGG Oy 241 TGGGTGTGG

Prc

Db 1321 TGCCTTGGCTGACTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1380 Qy 1381 TCCTTGCATCCCAGCTGATCCCTGCCAGGGCCCTTCCTTC	Application US/10104047 US20030236392A1 ATION: UX RESEARCH INSTITUTE WITON: NO. US20030236392A1e1 full length cDNA WITON: NO. US20030236392A1e1 full length cDNA S: H1-A0105 SATION NUMBER: US/10/104,047 STON NUMBER: ID NOS: 4096 ant In Ver. 2.1	Query Match 98.8% Score 1692.8; DB 6; Length 1785; Best Local Similarity 99.9%; Pred. No. 0; 3. Indels 0; Gaps 0; Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 ATGCCCCGCCCTCGACCCCCGCCACACTTGGGCCTCCACGCTTGGGAGGGGGGGG	Db 150 CGCCAACAGACTATGTTTTTTTTTTTTTTTTTTTTTTTT	181 ATCTGGCTCTCCTGAGCCGCCCTTGAGTCCCCACCTGCTGCTTGCGCGACCC 240 181 ATCTCTGGCTTGCTGCTGCCTGCTGCTGCGCGACCC 240 181
			1081 ATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1140 1141 TTCCAGGGCACCGACACACACGCGGGGGCCCCTTGCTCCAGGTGTGCTAACCC 1200 1141 TTCCAGGGCACCGACACACACGCGGGGGGCACCCTTGCTCCAGGTGTACTGCTAACCC 1200 1141 TTCCAGGGCACCGACACAGACTCGTCGGGGGGCACCCTTGCTCCAGGTGTAACTGCTAACCC 1200	1201 CTGCCAGGCCAGCACACACTTCTGGGAAAGCATGGCCTACAGAATGAAGAGGG 1260

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390 CGCTGTGGAGCCTGTGTGCGGGATGCCAGCCCTGCCTGTCTACTGAGGACTCCACTGAG 449 361 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCCGGCCTGATCGT 420	OY 1441 TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 1500
21 GCACCCCCAGCGGGGTGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC	OY 1501 ACTCCATCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTTGGGGTAAT 1560
TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCGGGGCCACCACCACTACCCCAATTAAGCTCCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCAATTAAGCTCAAAGAATCATCCTGTGTATAACTTATCTAAAGAATCATCCTGAAAGAAA	Oy 1561 TCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGGATTGGGGGGTGGGCCCACT 1620
GCCCTGATGCGGACTCCTGCTGCAGGGGCATGGCCGATCCCCCACCCA	OY 1621 CTATGTTATGTTAGGAGTTGGTTCTTGGCTGATGTTCTGTATCTTAACATGAC 1680
AGCCTGCCCAGCACTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT	Oy 1681 CACAGTTTGTAAGTAC 1696
661 GAGTCGGACCTGGACCTGCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT 720 	
721 GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGACTGGCC 780 	40
781 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 840 	; APPLICANT: Chen, Sel-Yu ; APPLICANT: Liu, Yongming ; APPLICANT: Liu, Chenghua ; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
841 AGCATCACGCAGGACTACCACCTGGATGAGCAGTGCTGAGGGCCGCCTGGTACGCGGC 900 	; FILE REFERENCE: DEX-0291 ; CURRENT PELLICATION NUMBER: US/09/989,920 ; CURRENT FILING DATE: 2001-11-21 ; PRIOR APPLICATION NUMBER: 60/252,500
901 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA 960 	O)
961 ACTCGGGCTGCTGCCCCAACGGCTGCTGCCCCTGACATGGCCATGAGACCATGGTGGGC 1020	; LENGTH: 1977 ; TYPE: INTERNATION HOMO Bapien ; ORGANISM: HOMO Bapien US-09-989-920-56
1021 TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCC 1080 	Query Match Best Local Similarity 99.0%; Pred. No. 0; Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;
1081 ATCGCCCGGAAGCTCAGGCCTTATGCAGCTCCAGGGTACCCAGCAGCCATGACTCATCC 1140 	OY 1 ATGCCCGCCTGGACACCCCGCCCACATCTGGGCCTCCACGATCTGGGACCTGGGGG 60
1141 TTCCAGGGCACCGACACACACTCGTCGGGGGCACCCTTGCTCCAGGTGTACTGCTAACCC 1200 	QY 61 CGGCCAACAGAGTATGTCTGGAGACATATGATAAACCACCTCAGCCCCACCAAGCCGC 120 Db 314 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCACCAAGCCGC 373
1201 CTGCCAGGCCCAGCTGCCACACTTTCTGGGAAAGCATGGCCTACAGAATGAAGAGGG 1260 	OY 121 CGCACCCGTAGACCACAACCCCAAGGACCCTTGGGCCAGAGAGCATTACCTTC 180
1261 GGACCAGGAACCCCTGTGGGAGAGACTTAGAACTGAAGCAGTGCCCACTCTGGCTCCTCC 1320 	OY 181 ATCTCTGGCTCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTGGCGACCC 240
1321 TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1380 	QY 241 TGGGTGTGGGGGTGCTGCCGGGCTTCTGCTTCCG-CCGCTGCGGGATTGCCTCCA 299 Db 494 TGGGTGTGGGGGTGCCGGGCTTCTGCTTCTGCTTCCGCCG
1381 TCCTTGCATCCCCAGCTGGTCTGATCCCTGCCAGGGCCCCTTCCTT	Oy 300 GCGCTGTGGA-GCCTGTGTGCGGGATGCAGCCCTGCCTGCTGACTGAGGACT-CCACT 357

Qy 1430 GCTCATGGTCTTCAGGTGATCATGGAAAGTAAGGCATTACCTTCTGGG 1489 Db 1694 GCTCATGGTCTTCAGGTGCCTGATCATGGAAAGTAAGGCATTACCTTCTGGG 1753 Qy 1490 AGTGAACCCTGACTCCCTCATTGCCACCAACTTCTCCCTC 1549 Db 1754 AGTGAACCCTGACTCCATTGCCACCCTAACCAACTTTCTCCCTC 1813 Qy 1550 CCTGGGGTAATTCAACTTAAAAGAAGCTTAATCTTAAATGTAATTGGGGGTGGG 1609 Db 1814 CCTGGGGTAATTCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGGGGGTGGG 1803 Qy 1610 CAGGGCCCACTCTATGTTAAAGAGCTTATCTTAAATGTATTGGGGGGTGGG 1803 Qy 1610 CAGGGCCCACTCTATGTTAAAGAGGTTGGTTCTGGTTCTTGGCTGATGTTCTGTAT 1669 Db 1874 CAGGGCCCACTCTATGTTAATGTTAAGGAGTTCTGGTTCTTGGCTGATGTTCTGTAT 1933 Qy 1670 CTTAACATGACCACAGTTTATGTTAAGTACTCTGGTTCTTGGTTCTTGTAT 1933 Qy 1670 CTTAACATGACCACAGTTTGTAAGTACCTCGGCCGCGCCCACCCA	RESULT 4 US-09-989-920-117 Sequence 117, Application US/0998920 Sequence 117, Application US/0998920 Sequence 117, Application US/0998920 Patent No. US2002017257A1 APPLICANT: Macina, Roberto APPLICANT: Recipon, Herve APPLICANT: Chen, Sel-Yu APPLICANT: Chen, Sel-Yu APPLICANT: Liu, Chengaitions and Methods Relating to Lung Specific Genes FILE REFERENCE: DEX-0291 CURRENT APPLICATION NUMBER: US/09/989,920 CURRENT APPLICATION NUMBER: US/09/989,920 CURRENT FILING DATE: 2000-11-22 NUMBER: OF SEQ ID NOS: 284 SEQ ID NO 117 LENGTH: 1977 TYPE: DAA COSCHARE: PatentIn version 3.1 SEQ ID NO 117 LENGTH: 1977 TYPE: DAA COSCHARE: Homo sapien US-09-989-920-117	Query Match 93.5%; Score 1602.4; DB 3; Length 1977; Best Local Similarity 99.0%; Pred. No. 0; Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9; Qy 1 ArdCCCGCCCTGCACCCCGCCCAGCATCTGGGCCTCCAGCCTTGGGACCGTGGGAG 60 Db 254 ATGCCCGCCCGCCCGCCCAGCATCTGAGACCTCCACCCTCAGCCCTCAGGCCGTGGAG 313 Qy 61 GGGCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGGAGG 513 Db 314 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGAGCGC 373 Qy 121 CGCACCCGTAGACCCCCAAGGACCTTGAGTCCACCTCAGCCCCCACCAGGCGC 373 Qy 121 CGCACCCGTAGACCCCAAGGACCCTTGAGTCCCCCACTGGGCCACAGGAGACATTACCTTC 433 Qy 181 ATCTCTGGCTCTGCTGAGCCCCCTTGAGTCCCCCACTGGGCCACTGGCGCCCCCCCACTGGCGACCCTCTGCTGCTGCTCTCGCGGACCCCCACTGGCGCCCTCTGGCGCCTCTTGGCGCCCCCCCC
Qy 358 GAGGGACTGCTGAACTGG-GCCAAGGAGCACAATGGAGTGCCCCCAGCCCTGA 416 bb 614 GAGGGACTGCTGAAGCCAACTGGAGCACAATGGAGTGCCCCCCAGCCCTGA 673 C17 TCGTGACACCCCCCAGCCCAGCGAGGAGCCAATGGAGTCCACCTCAACTCACCTCAGCCCTGA 472 Qy 417 TCGTGACCCCCCAGACCGCGAGTGGCCAAGCGGCTCAACCCATGGACACCATGGACACA 733 Qy 473 GCTTCAGCTACCCCGAGCGAGCGAGCGCAGGCGAGCCTCCTGTGTATCCCTACCCGAGGCGC 733 Qy 473 GCTTCAGCTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCC 793 Qy 532 ACCTCCCCAGCCCCTAATGCGGACTCCTGCTGATGTCCCTACCCGAGAGGCC 793 Qy 532 ACCTCCCCAGCCCTGATGTTAAGCTCTGCTGCAAGGACCACTGGCCGATCCCCCACCC 883 Qy 592 ATGCGA-CACCAGCACCTTGCTGCTCCTGTGTACTCCCCACCCCCCCC		000 000

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	RESULT 5 US-10-074-475-124 Sequence 124, Application US/10074475 Sequence 124, Application US/10074475 Sequence 124, Application No. US2003009289&1 GENERAL INFORMATION: APPLICANT: Salceda, Susana APPLICANT: Hu, Ping APPLICANT: Rarra, Kalpana APPLICANT: Rarra, Kalpana APPLICANT: Cafferkey, Robert APPLICANT: Liu, Chenghua TITLE OF INVENTION: Genes and Proteins FILE REFERENCE: DEX-0313 CURRENT APPLICATION NUMBER: US/10/074,475 FRIOR PILING DATE: 2001-02-13 PRIOR FILING DATE: 2001-02-13 FRIOR FILING DATE: 2001-02-13	Query Match 35.5%; Score 607.6; DB 5; Length 654; Best Local Similarity 96.6%; Pred. No. 5.1e-178; Matches 632; Conservative 0; Mismatches 19; Indels 3; Gaps 1; QY 89 ArgaraaaCcaccacaccacacacacacacacacacacacaca
358 GAGGGACTGCTGAAGCCAACTGG-GCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGA 416 614 GAGGGACTGCTGAAGCCAACTGGTGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGA 673 417 TCGTGCACCCCCCAG-CCGGCGGAATGGCCAGCGGCTCAAGTCAACCATGGGCAGCA 772 674 TCGTGCACCCCCCAG-CCGGCGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCA 733 675 TCGTGACTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCGGGCAGCA 733 676 TCGTGACTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAG-GGCC 531 677 TCGTGCACCCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGAGGCC 793 678 TCGTCACCCCAGCCCTGATGCGGATCCTGCAAGGAGCCACTGGCCGATCCCCCACCC 591 679 ACCTCCCCCAGCCCTGATGCGGACTCCTGCAGAGAGCCACTGGCCAACCCCCACCC 853 670 ACCTCCCCCAGCCCTGATGCGCAACTCCTGCTGAAGGACCACTGGCCAACCCCACCC 853 671 ACCTCCCCCAGCCCTGCAAGCAACTCCTGCAAGGACCACTGGCCCATCCCCCACCC 853 672 ATGCGA-CACACCCTGCCAGCACCCTTTGCCAAGAGACCCCTTGGCCAGAGATACTA 650 674 ATGCGA-CACACCCTGCCAGCACCTTTGCCAAGAGCCCCCTGGGGAGTACTA 650 674 ATGCGAACACACCCTTTGCCAAGAACCCTCGTGGCTCCCGAGGAGTACTA 913	651 TTCTTTCCATGAGTCGGACCTGCGGAGATGGCCAGTGGCTCCATGTCGAGCCG 710 914 TTCTTTCCATGAGTCGGACCTGCCGGAGATGGCCAGTGGCTCCATGTCGAGCCG 973 711 AGAAATTGATGTCGCTCATCTTCAAGAAGTCGACAGTGCGCTACACCAGATCG 769 974 AGAAATTGATGTCTCATCTTCAAGAAGTCTGACAGAGCTTCAGGCTACACCAGATCG 769 975 AGAAATTGATGTCTCATCTTCAAGAAGTCTGACAGAGCTTCAGGCTACACCAGATCG 1033 770 ATGAGTTGACTCATCTTCAAGAAGTCTGTTCCTGGAGAAGACCAGTAAGATCTCGG 1033 770 ATGAGTTGACGCCAAGTGCACATCAGACACTGTTCCTGGAGAAGACCAGTAAGATCTCGG 1093 830 ACCTTATCAGCAAGACATCAGACACTGTTCCTGGAGAAGACCAGTAAGATCTCGG 1093 830 ACCTTATCAGCAAGACATCAGACACTACACACACACACAC	1070 CTGCAGATGCCATCGCCCGGAAGCTGAAGCCTTATGGAGCTCCAGGCTACCCAGCAAGCC 1129

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Best Local Similairy ....
Matches 569; Conservative
                                                           Local Similarity
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                                                                                                                                           TCCCTGTGTATCCCTACCCGAGGCCACCTCCCCAGCCCCTGATGCGGACTCCTGCTGCA 565
                                                                                                                                                                  421 TCCCTGTGTATCCCTACCGAGAGGCCACCTCCCCCAGCCCCTGATGCGGACTCCTGCTGCA 480
                                                                                                                                                                                                                                     481 AGGAGCCACTGGCCGATCCCCCACCCAGCGAGCAGCCTGCCCAGCACCTTGCCAGTA 540
                                                                                                                                                                                                                                                                                                                       Sequence 5731, Application US/10779543

Publication No. US20050227917A1

Sequence 5731, Application US/10779543

Publication No. US20050227917A1

Sequence 5731, Application US/107791

Publication No. US20050227917A1

APPLICAMY: Williams et al

TITLE OF INVENTION: GENE PRODUCTS DIPPERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

FILE REFERENCE: 2300-21302

CURRENT APPLICATION NUMBER: US/10/779,543

PRIOR PRIJING DATE: 1998-12-21

PRIOR PELING DATE: 1998-12-23

PRIOR PELING DATE: 1998-10-21

PRIOR PELING DATE: 1998-10-21

PRIOR PELING DATE: 1998-10-21

PRIOR PELING DATE: 1998-10-21

PRIOR PELING DATE: 1998-01-28

PRIOR PELING DATE: 1998-01-38

PRIOR PELING DATE: 1998-01-38

PRIOR PELING DATE: 1998-03-31

PRIOR PELING DATE: 1998-03-31
                                                     447 -GCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGCTACCCCGATGTTAAGCTCAAAGGCA
                                                                                    361 CGGCTGCAAGTCAACCATGGGCAGCAGCTTCAGCTACCCCGATGTTAAGCTCAAAGGCA
                                                                                                                                                                                                                       566 AGGAGCCACTGGCCGATCCCCCACCCATGCGACACAGCCTGCCCAGCACCTTTGCCAGTA
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LOCATION: 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 20,
LOCATION: 22, 23, 24, 25, 28, 29, 30, 36, 41, 85, 89, 97, 106, 108,
LOCATION: 115, 134, 139, 177, 185, 207, 232, 275, 283, 303, 320, 327,
LOCATION: 356, 414, 451, 459, 551, 566, 582, 588, 591, 605, 631, 656
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM, NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5731
                                                                                                                                                                                                                                                                                                                                                                                 TGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGATGTGCTCATCTTCAAGAAGC
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NAME: NAME: Misc feature
LOCATION: 661, 678, 681, 687, 689, 702, 706, 710, 711, 713,
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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US-10-779-543-5731
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GENERAL INCOMPANTATION:

APPLICANT: Recipon, Herve

APPLICANT: Recipon, Herve

APPLICANT: Commons

APPLICANT: Change and Methods Relating to Lung Specific Genes and Prote

TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote

FILE REPRENCE: DEX-0291

CURRENT APPLICATION NUMBER: US/09/989,920

CURRENT APPLICATION NUMBER: US/09/989,920

CURRENT APPLICATION NUMBER: 05/0252,500

PRIOR FILING DATE: 2000-11-22

NUMBER OF SEQ ID NOS: 284

SOFTWARE: Patentin version 3.1

SEQ ID NO 55

LENGTH: 385

TENET: DNA

ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            568 AGTGCCCACTCTGGNTCCTCNTGNCTTGGCTGACTGGNTT-CTGGACCATGTGCATTTCA
                                                                                                                                                                                                                        GGCCGCCTGGTACGCGCCATCATTCGCATTAGTACCCGAAAAGAGCCGTGCTCGCCCACA
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                                                                                                                                                GGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTAATGGAGCTCCAGGGTACCC
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Length 728;
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DB 9;
27.0%; Score 463.2; DB 9;
88.4%; Pred. No. 4.6e-133;
ive 0; Mismatches 66;
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APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILE REPRENCE: DEX. 2013
CURRENT APPLICATION NUMBER: US/10/074,475
CURRENT FILING DATE: 2002-02-13
FRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 295
SEQ ID NO 123
LENGTH: 386
                                                         1435
                                                                                                                                                                                                             1196 AACCCCTGCCAGGCCCAGCTGCCACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAA 1255
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                 122 cerecerecerresereserreserrecesecarersearreseresesecarsesarer 181
                                                                                               2 ACCCTGGCCAGGCCCAGCTGCCAACCCTTTCTGGGAAAGAAGGATGGCCTACAGAATGAA
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                                                         62 GAGGGGGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCT
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                                                                                                                                                                                                                                                                                        1556 GTAATTCAACAGTTAAAAGAAGCTT 1580
                                                                                                                                                                                                                                                                                                            362 GTAATTCAACAGTTAAAAGAAGCTT 386
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 123, Application US/10074475; Publication No. US20030092898A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
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Publication No. US20040166105A1

GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Pluta, Jason
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and ITLE REFERENCE: DEX-0287
CURRENT FILING DATE: 2001-11-21
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                                                                                                                 1190 ACTGCTAACCCCTGCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCCTACAG 1249
                                                                                                                                                                                             1250 AATGAAGAGGGGGACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACT 1309
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                                         DB 3; Length 385
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                                     22.5%; Score 385; DB 3;
100.0%; Pred. No. 8e-109;
tive 0; Mismatches 0
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PRIOR APPLICATION NUMBER: 60/252,509
PRIOR FILING DATE: 2000-11-22
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SOFTWARE: PatentIn version 3.1
                                       Query Match 22.5
Best Local Similarity 100.
Matches 385; Conservative
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Matches 382; Conservative
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ORGANISM: Homo sapien
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US-09-989-890-104
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   US-09-989-920-55
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LENGTH: 386
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    261 ACAGTGCAGATCTCCCAGGACACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTAT 320
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Publication No. US20050227917A1
GENERAL INCPRANTION:

APPLICANT: Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: UN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302
CURRENT APPLICATION NUMBER: US/10/779,543
CURRENT FILING DATE: 2002-02-12
FRIOR PILING DATE: 1998-12-21
FRIOR APPLICATION NUMBER: 60/068,755
FRIOR PILING DATE: 1999-12-21
FRIOR APPLICATION NUMBER: 60/068,755
FRIOR APPLICATION NUMBER: 60/105,234
FRIOR PILING DATE: 1998-04-03
FRIOR PILING DATE: 1998-04-03
FRIOR PILING DATE: 1998-04-03
FRIOR PILING DATE: 1998-04-03
FRIOR PILING DATE: 1998-01-28
FRIOR PELING DATE: 1998-01-28
FRIOR PELING DATE: 1999-01-28
FRIOR APPLICATION NUMBER: 60/072,910
FRIOR PELING DATE: 1998-01-28
FRIOR PELING DATE: 1
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Pred. No. 5.6e-97;
0; Mismatches 1; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-12051
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Best Local Similarity 99.7%;
Matches 347; Conservative
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FEATURE:
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US-10-7/9-543-100966
US-10-7/9-543-100966
Publication No. US2005027917A1
GENERAL INFORMATION:
APPLICANT: Williams et al
TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302
CURRENT FILING DATE: 2004-02-12
CURRENT FILING DATE: 100706,555
PRIOR PELICATION NUMBER: 09/217,471
PRIOR PELICATION NUMBER: 09/217,471
PRIOR PELICATION NUMBER: 00/066,755
PRIOR PELICATION NUMBER: 60/066,755
PRIOR PELICATION NUMBER: 60/066,755
PRIOR PELICATION NUMBER: 60/060,664
PRIOR PELICATION NUMBER: 60/080,664
PRIOR PELICATION NUMBER: 60/080,664
PRIOR PELICATION NUMBER: 60/105,234
PRIOR PELICATION NUMBER: 60/105,234
PRIOR PELICATION NUMBER: 60/02,910
PRIOR PELICATION NUMBER: 60/02,910
PRIOR PELICATION NUMBER: 60/072,910
PRIOR PELICATION NUMBER: 60/090,114
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Pred. No. 9.8e-99;
0; Mismatches 5;
                                                                                                                    1556 GTAATTCAACAGTTAAAAGAAGCTT 1580
                                                                                                                                                                     362 GTAATTCAACAGTTAAAAGAAGCTT 386
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; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-10096
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20.6%;
Best Local Similarity 98.4%;
Matches 366; Conservative
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ORGANISM: Homo sapiens
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241 GACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGC 300
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APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Jones, Lee William
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
ITILE OF INVENTION: Novel Human Genes and Gene Expression
ITILE OF INVENTION: Novel Human Genes and Gene Expression
FILE REPERENCE: 2300-1480
CURRENT APPLICATION NUMBER: US/10/076,555
CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/217,471
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/068,755
PRIOR PILING DATE: EARLIER FILING DATE: 1998-12-21
PRIOR PLILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR PLLING DATE: EARLIER FILING DATE: 1998-10-21
PRIOR PLLING DATE: EARLIER FILING DATE: 1998-10-21
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-27
NUMBER OF SEQ ID NOS: 844
SEQ ID NO 34
LENGTH: 300
LENGTH: 300
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                                                                                                                                                                                                                             APPLICANT: Williams, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Innis, Wichael A.
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Sudduth-Klinger, Unlie
APPLICANT: Reinhard, Christoph
                                                                                                                                                     Sequence 34, Application US/10076555 Publication No. US20030065156A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crkvenjakov, Radomir
Dickson, Mark
Drmanac, Snezana
                                                                                                                                                                                                                                                                                                                                                                                                            Randazzo, Filippo
Kennedy, Giulia C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Labat, Ivan
Leshkowitz, Dena
Kita, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pot, David
Kassam, Altaf
Lamson, George
Drmanac, Radoje
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ORGANISM: Homo sapiens
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                                                                                                               320 TGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG 379
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US-10-779-543-1705

Sequence 1705, Application US/10779543

Publication No. US20050227917A1

GENERAL INFORMATION:

APPLICANT: Williams et al

TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

FILE REPERSNCE: 2300-2130

CURRENT FILING DATE: 2004-02-12

PRIOR APPLICATION NUMBER: 09/21/471

PRIOR APPLICATION NUMBER: 00/068,755

PRIOR APPLICATION NUMBER: 60/068,755

PRIOR PLING DATE: 1998-04-03

PRIOR PLING DATE: 1998-01-28

PRIOR PLING DATE: 1998-01-28

PRIOR PLING DATE: 1998-01-28

PRIOR PLING DATE: 1998-02-4

PRIOR PLING DATE: 1998-03-31

PRIOR PLING DATE: 1998-03-31

PRIOR PLING DATE: 1998-03-31

REACH APPLICATION NUMBER: 60/000,114

PRIOR PLING DATE: 1998-03-31

PRIOR PLING DATE: 1998-03-31

Remaining Prior Application data removed - See File Wrapper or PALM.

SCOTT NAO-1706.
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17.5%; Score 300; DB 9; I
Best Local Similarity 100.0%; Pred. No. 2.1e-82;
Matches 300; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                               US-10-779-543-1705
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LENGTH: 300
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Gaps

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Search completed: March 11, 2006, 22:42:56 Job time: 1289 secs
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980 CCGCTGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGCTCAGGTCTCAGGCCAGGATG 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    860 ACCTGGATGAGCAGGATGCTGAGGCCCGCCTGGTACGCGGCATCATTCGCATTAGTACCC 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              920 GAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAA 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGACAGAGCTGTTCAGCGTACACAGATCGATGAGCTGGCCAAGTGCACATCAGACACTG 60
                                                                                                                                                                           Sequence 34, Application US/10779543

Publication No. US20050227917A1

Publication No. US20050227917A1

Publication No. US20050227917A1

APPLICAMY: Williams et al

TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

FILE REFERENCE: 2300-21302

CURRENT FILING DATE: 2004-02-12

PRIOR APPLICATION NUMBER: US/10/779,543

PRIOR FILING DATE: 1998-12-21

PRIOR APPLICATION NUMBER: 60/066,755

PRIOR PRILING DATE: 1998-12-23

PRIOR FILING DATE: 1998-10-21

PRIOR FILING DATE: 1998-10-21

PRIOR FILING DATE: 1998-10-21

PRIOR FILING DATE: 1998-10-21

PRIOR PELING DATE: 1998-01-28

PRIOR PELING DATE: 1998-01-28

PRIOR FILING DATE: 1998-01-28

PRIOR PELING DATE: 1998-01-38

PRIOR PELING DATE: 1998-03-34

PRIOR PELING DATE: 1998-03-34

PRIOR PELING DATE: 1998-03-31

PRIOR PELING DATE: 1998-03-31
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NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                      RESULT 14
US-10-779-543-34
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LENGTH: 300
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RESULT 15 US-09-989-920-116/c

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; Sequence 116, Application US/0998920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Yongming
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0291
; CURRENT FILING DATE: 2001-11-21
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR APPLICATION NUMBER: 60/252,500
; NUMBER OF EGG ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; TENGRA 10-16
; TENGRA 10-16
; TENGRA 10-16
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100.0%; Pred. No. 1.6e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Sequence 13469, A Sequence 2307, Ap Sequence 73, Appl Sequence 73, Appl Sequence 73, Appl Sequence 74, Appl Sequence 13376, A Sequence 31877, A Sequence 55078, A Sequence 55078, A Sequence 55078, A Sequence 6517, Appl Sequence 6517, A Sequence 641562, Sequence 641562, Sequence 56117, A Sequence 56117, A Sequence 56117, A Sequence 56117, A Sequence 24337, A Sequence 2433

Sequence 485, App Sequence 485, App

OM nucleic

Run on:

Sequence:

Searched:

Database

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DB 9; Length 1785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-330-773-159
US-10-750-185-56117
US-10-750-623-56117
US-10-330-773-242
US-09-925-065A-841922
US-10-750-185-24937
                                                                                                                                                                                                                                                                                                                                                              US-11-136-527-2597
US-09-925-065A-535967
US-09-925-065A-681562
                                                                                                                                          US-10-517-544-76
US-10-995-561-13376
US-10-750-185-31877
US-10-750-623-31877
US-10-750-623-55078
US-10-750-623-55078
US-11-072-512-977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-750-623-24937
US-10-973-115B-485
US-10-131-826A-485
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Pred. No. 0;
0; Mismatches
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APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUTA, MACOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/072,512 CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: UP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SEQ ID NO 799
LENGTH: 1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 799, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTSÚKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.8%;
Best Local Similarity 99.9%;
Matches 1694; Conservative
                         138627
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CORGANISM: Homo sapiens
US-11-072-512-799
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                                                                                                                                                                       March 11, 2006, 20:00:54; Search time 591 Seconds (without alignments) 6687.647 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/USOS_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/USOS_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

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7: /cgn2_6/ptodata/2/pubpna/USOS_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/USOS_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/USI_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/USI_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna/USI_NEW_PUB.seq:*

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13: /cgn2_6/ptodata/2/pubpna/USII_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/USII_NEW_PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2 US-11-124-368A-156
2 US-11-124-368A-156
US-09-925-065A-893863
US-09-925-065A-894029
2 US-11-052-554A-519
2 US-11-096-56A-2110
US-10-330-773-603
US-10-522-077-2
US-10-925-065A-551694
2 US-11-121-086-72
US-09-925-065A-56292
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US-09-925-065A-56292
US-09-925-065A-56292
US-10-995-561-314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7673375 segs, 1153648444 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - nucleic search, using sw model
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Maximum DB seq length: 200000000
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1713
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CGGCCAACAGGCTATGTCTGGAGACATATGATAAACCTCTCAGCCCCCCCC	1230 TTCCAGGGCACCGACAGACTCGTCGGGGGCCACCTTGCTCCAGGTGTAACTGCTGACCCCTTGCTCCAGGTGTAACTGCTGACCCCCTTGCTCCAGGTGTAACTGCTGAGCCCCCCCTTGCTCCAGGTGTAACTGCTGAGAGGGGGGGG
CGCACCCGTAGACCCCAAGGACCCTGGCCACAGGGCCAGAGAGCATTACCTTC 269 ATCTCTGGCTCTGCTGAGCCGCTTGAGTCCCCCACCTGCCTG	DD 1290 CIGCCAGGCCCAGCTGCCACACCCTTTCIGGGAAGCATGGCCTACAGAAGGG 1349 QY 1261 GGACCAGGAACCCTGTGGGAAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTC 1320
ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTGCTGGCGACCC 329 TGGGTGTGGGAGTGCCGGGGCTGCCTTCTGCTTCCGCCGGGATTGCCTCCAG 300 TCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	OY 1321 TGCCTTGGCTGACTTCCTGGACCATGTGCATTTCACTGGGCATGGGATCTACATC 1380
	Oy 1381 TCCTTGCATCCCGGGTCTGATCCCTGCCAGGGCCCCTTCCTT
	QY 1441 TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 1500 Db 1530 TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGCCTTCTGGGAGTGAACCCTG 1589
	Qy 1501 ACTCCATCCCCTATTGCCACCTAACCAATCATGCAAACTTCTCCCTCGGGGTAAT 1560
	QY 1561 TCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATT
60	OY 1621 CTATGTTATGTTAAGGAGTTGGTTCTTGGCTGAAGTTCTGTATCTTAACATGAC 1680 1710 CTATGTTAAGGAGTTGGTTCTTGGTTCTTGGCTGATGTTCTTGTACTTAACATGAC 1769
	OY 1681 CACAGITTGTAAGTAC 1696 Db 1770 CACAGITTGTAAGTAC 1785
GAGTCGGACCTGGACGAGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT 720 	RESULT 2 US-10-501-035-144 ; Sequence 144, Application US/10501035
GTGCTCATCTTCAAGAAGCTGAACAGTTCAGCGTACGACTGGATGAGCTGGCC 780 	4 0
aagtgcacatcagacactgtgttcctggagaagaccagtaagatctcggaccttatcagc 840 	; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASES; TILLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS; FILE REFERENCE: D0108 PCT; FILE REFERENCE: D0108 PCT; CURRENT APPLICATION NUMBER: US/10/501,035
AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGC 900	
ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCACAGACCTCGGAGGGTCGTTCA 960 	SBS
ACTCGGGCTGCTCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGC 1020	ens 2.4%;
TCAGGTCTCAGCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCC 1080 	Similarity 4; Conservat TGCCCGCCCTC
114	18

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TYPE: DNA
CORGANISM: Homo sapiens
US-11-124-368A-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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US-11-124-368A-155
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Sequence 154, Application US/11124368A

Publication No. US20050287559A1

GENERAL INFORMATION:

APPLICANT: Michele Cargill

APPLICANT: May Luke

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

FILE REFERENCE: CL001524

CURRENT APPLICATION NUMBER: US 60/568,845

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-01-09

NUMBER OF SEQ ID NOS: 21112

SOFTWARE: FastSEQ for Windows Version 4.0
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CORGANISM: Homo sapiens
US-11-124-368A-154
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LENGTH: 3320
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RESULT

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Sequence 155, Application US/11124368A
; Sequence 155, Application US/20050287559A1
; Bublication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Wascular Diseases, Methods of Detection and Uses Thereof
; FILE REPERBENCE: CLO01524
; CURRENT APPLICATION NUMBER: US/01/1/124,368A
; CURRENT PAPLICATION NUMBER: US 60/568,845
; PRIOR APPLICATION NUMBER: US 60/655,936
; PRIOR PILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: US 60/655,936
; PRIOR PILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTHARE: PRESEQ for Windows Version 4.0
; SEQ ID NO 155
LENTH: 3.422
Sequence 156, Application US/11124368A

Publication No. US20050287559A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: May Luke
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REPRENCE: CLOUSE24

CURRENT APPLICATION NUMBER: US/11/124,368A

CURRENT FILING DATE: 2005-05-09

PRIOR APPLICATION NUMBER: US 60/568,845

PRIOR APPLICATION NUMBER: US 60/568,845

PRIOR PLING DATE: 2004-05-07

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 21112

SEQ ID NOS: 21112

SEQ ID NO 155-05-07

SEQ ID NO 155-05-07

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SEQ ID NO 155-05-07
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AGCTGGCCAAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACC 832
                                                                  275 Aregearegeadecacegegecregeseregecearecerecereceageareseraceaac 334
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US-09-925-065A-894029/c
Sequence 894029, Application US/09925065A
; Sequence 804029, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT PELICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
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                                                                                                                                         TTATCAGCAGCATCACGCAGGACTACCACCTGGA
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Pred. No. 1.9;
0; Mismatches
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Best Local Similarity 50.3%;
Matches 95; Conservative
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US-09-925-065A-893863
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US-11-052-554A-519/C

US-11-052-554A-519/C

Sequence 519, Application US/11052554A

Publication No. US20050288866A1

GRNERAL INFORMATION:

GRNERAL INFORMATION:

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL

CURRENT PILING DATE: 2005-02-07

PRIOR FILING DATE: 2004-02-07

PRIOR FILING DATE: 2004-07-07

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: PatentIn version 3.3

SEQ ID NO 519
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50.3%; Pred. No. 1.9;
cive 0; Mismatches 94; Indels
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Pred. No. 3.8;
0; Mismatches 119;
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PELING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 894029
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ORGANISM: Mycobacterium tuberculosis H37Rv
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Best Local Similarity 48.0%;
Matches 110; Conservative
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nes 95; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-894029
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                                                                                                           11 CTGGACACCCCCCCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAGCGGCCAACAG
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; Sequence 603, Application US/10330773
; Publication No. US20060040262A1
; GABERAL INFORMATION:
   APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 603
; LENGTH 38239
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   ilarity 43.3%; Pred. No. 4.7;
Conservative 0; Mismatches 229; Indels
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2.2%; Score 37.6; DB 7;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 94; Conservative 0; Mismatches 94;
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Best Local Similarity
Matches 175; Conserv
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US-10-330-773-603
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Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: 275-159220C5

CURRENT PELICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 22110

LENGTH: 1431
5670 ecécricrereréecrecrerécricérecrérasccéséccaecrerrecrecaécae 5611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION UNDER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                  1927 ecceccecceareccerreccircrrecareaceccecererecce 4879
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                                                                                                               283 TGCCGGGATTGCCTCCAGCGCTGTGGAGCCTGTGTGCGGGGATGCAGCC 331
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Pred. No. 8.6;
0; Mismatches 107; Indels
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LOCATION: (1). (1). (1431)
OTHER INFORMATION: Ceres Seq. ID no. 12407603
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                                                                                                                                                                                                                                                                                                                                                         Sequence 306, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mays
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; ORGANISM: Rattus norvegicus
US-11-136-527-306
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Matches 102; Conservative
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US-11-096-568A-22110/c
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US-11-136-527-306/c
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Sequence 200, Application US/10501035

Publication No. US20060046249A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLECTIDES AND POLYPEPTIDE FOR PREDICTING

TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INVERACT WITH PROTEIN TYROSINE KINASES

TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158170 CCAĞGTĞCAĞTĞĞÇTCATGAÇÇTATAAGAĞATCCTCAGGĞĞATCCTCCTĞCCTTĞĞCTTC 158229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 72, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: UNCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
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Pred. No. 5.5;
1; Mismatches 144; Indels
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Best Local Similarity 57.9%; Pred. No. 26;
Matches 66; Conservative 0; Mismatches
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Matches 136; Conservative
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; LENGTH: 1067
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-551694
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              Sequence 2, Application US/10522037

Sequence 2. Application US/10522037

Publication No. US20050282166A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Cells.

TITLE OF INVENTION: Cells.

FILE REPERINCE: B0149WO

CURRENT APPLICATION NUMBER: US/10/522,037

CURRENT FILING DATE: 2005-01-24

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1

SEQ ID NO 2.
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PUBLICATION NO. US20040181048A1

FURDICATION NO. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-11-6

PRIOR PRILING DATE: 2001-01-6

PRIOR FILING DATE: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: DNA sequence of clone FS3-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial sequence
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5748 GCCCAGAAGCACGTTGGCAACATGGTGAGGCTGCCCAGTGTTCAGCGCAAAG 5696
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FILE REPERENCE: D0185 PCT
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
FRIOR APPLICATION NUMBER: US 60/350,061
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE: PatentIn version 3.2
LENGTH: 6034
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GRGANISM: Homo sapiens
US-10-501-035-200
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Query Match 100.0%; Score 1713; DB 6; Length 1713; Best Local Similarity 100.0%; Pred. No. 0; No. 0; Anarches 1713; Conservative 0; Nismatches 0; Indels 0; Gaps 0; Qy 1 ATGCCCCGCCCTGGACACCCCGGCCAGCATCTGGGCCTCCAGGTTGGGACGTGGGG 0 Db 1 ATGCCCCGCCTGGACACCCCGCCCGCCCAGCATCTGGGCCTCCAGGTGGGG 0 Qy 61 CGGCCAACAGGCTATGTTGTGGACATATGATAAACCACCTCAGCCCCCAACCGC 120 Db 61 CGGCCAACAGGCTATGTTGTGATAAACCACCTCAGCCCCCAACCAGCCG 120	121 CGCACCGTAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC 1	DB	361 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT 4	DECECTOR	Qy 601 AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGAGGAGTACTATTCTTTCCAT 660	Db 661 GAGTCGGACCTGCCGGAGATGGGCCGTGGTCTTGTTGTTTTTTTT	OY 781 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 840	Oy 841 AGCATCACGAGGACTACCACTGGATGAGCAGGATGCTGAGGGCCGCTCGTACGGGC 900 Db 841 AGCATCACGCAGGACTACCACCTGGATGCTGAGGGCCGCCTGGTACGCGGC 900 Oy 901 ATCATTCGCATTAGTACCCGAAGGCCGTCGTCGCCCACAGACGTCGTTCA 960 Db 901 ATCATTCGCATTAGTACCCGAAGGCTCGCTCGCCCCACAGACCTTCGAAGGCTCGTTCA 960 Oy 961 ACTCGGGCTGCTCGCCCCCCCCCCCCCCCCCCCCCCCCC

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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Boufferd, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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through the I.M.A.G.B. Consortium/LinL at: http://image.llnl.gov
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/db_xref="GeneID:126695"
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/clone="MGC:45763 IMAGE:3960220"
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/clone lib="NHH MGC 21"
/lab_host="DH10B-R"
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	1277 TGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCCTGCCTTGGCTGACTTGG 1201 TGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCCTGCCTTGGCTGACTGGCTGG	Oy 1337 GTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATCTCCTTGCATCCCAGC 1396	Qy 1397 TGGTCTGATCCCTGCCAGGCCCCTTCCTTCCTTCCTGCTCAGGTGGCCTGATCA 1456 Db 1321 TGGTCTGATCCCTGCCAGGCCCCTTCCTTCCTGCTCATGGTCTTCAGGTGGCCTGATCA 1380	QY 1457 TGGAAAGTAAGGGGTTTACCTTCTGGGAGTGAACCCTGACTCCCCTATT 1516 DD 1381 TGGAAAGTAAGGATTACCTTCTGGGAGTGAACCCTGACTCCCTATT 1440	OY 1517 GCCACCCTAACCATCATGCAAACTTCTCCCTCCTGGGGTAATTCAACAGTTAAAAGAA 1576 	QY 1577 GCTTATCTTAAATGTATTGGGGGGGGGGGCGCAGCCCACTCTATGTTAAGG 1636 DD 1501 GCTTATCTTAAATGTATTGTATTGGGGGGTGGGCCCACCCCACTCTATGTTATGTTAAGG 1560	Qy 1637 AGTTGGTTCTGGTTCTTGGCTGATGTTCTTGTAACATGACCACAGTTTGTAAGTAC 1696	RESULT 3 AX747274 LOCUS AX747274 AX747274 DEFINITION Sequence 799 from Patent EP1308459.	S	Hominidae; Homo. REFERENCE AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and	TITLE FULL-Length cDNA sequences JOURNAL Patent: EP 1308459-A 799 07-MAY-2003; Helix Research Institute (JP); Research Association for Biotechnology (JP) PRATURES	rce	ORIGIN Query Match Query Match Best Local Similarity 99.9%; Proceed, No. 0; Matches 1694. Conservative 0. Mismatches 2; Indels 0: Gans 0:	CCTGGACACCCCGCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG 60

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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamaterai, Kisarazu, Chiba 292-0812, Japan (64-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamaterai, Kisarazu, Chiba 292-0812, Japan (6-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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LLQVYC"
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PDPKDPGHHGPESITFISGSAEPALESPTCCLLWRPWWERAAFCFRCRDCLQRC
GACYRGCSPCLSTEDSTEGTABANWACEHNGVPPSPDRAPPSRDGQLKSTMGSSFS
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FHESDLDLPPEMGSGSMSSREIDVLIFKKLTELFSVHQIDELAKCTSDTVFLEKTSKIS
Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matuura, K., Nakaima, Y., Mizumo, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satch, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Okumura, K., Nakagawa, K., Okumura, K., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length
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/clone lib="KIDNE2"
/note="cloning vector: pME18SFL3"
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/organism="Homo sapiens"
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Nat. Genet. 36 (1), 40-45 (2004)
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/db_xref="taxon:9606"
/clone="KIDNE2015710"
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Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
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Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M.,
Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takashi,M., Kanda,K., Yokoi,T., Furuya,T., Kaku,
Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H.,
Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M.,
Hiraoka,S., Chiba,Y., Ishida,M., Kananabe,M., Watanabe,M.,
Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R.,
Takeuchi,K., Arita,M., Imose,N., Musahino,K., Yuuki,H., Oshima,A.,
Sasaki,N., Aotsuka,S., Yoshikawa,Y., Taksunay,H., Ichihara,T.,
Shiohata,N., Sano,S., Moniya,S., Momiyama,H., Ichihara,T.,
Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T.,
Sugiyama,A., Takewoto,M., Kawakami,B., Yamazaki,M., Watanabe,K.,
Kumagai,A., Tanigami,A., Fujiwara,T., Yamazaki,M., Watanabe,K.,
Tashiro,H., Tanigami,A., Fujiwara,T., Yamazaki,M., Watanabe,K.,
Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y.,
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                1230 TTCCAGGGCACCGACACAGACTCGTCGGGGGCACCCTTGCTCCAGGTGTACTGCTGACCC 1289
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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	RESULT 5 LOCUTIONS LOCUTION Sequence 3609 from Patent W002068579. ACCESSION COT17675 VERBION COT17675. GI:42278532 VERBION COT17675. I GI:42278532 VERBION COT17675. I GI:42278532 VERBION COT17675. I GI:42278532 VERBION COT17675. I GI:42278532 SOURCE ORGANISM Hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. TITLE Kite; Buch as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof JOURNAL Patent: W0 02068579-A 3609 06-SEP-2002; PEATURES Location/Qualifiers JOURNAL Patent: W0 02068579-A 3609 06-SEP-2002; PEATURES Location/Qualifiers SOURCE ADDIAGRAMMATCH OUT WAICH OUT WAI
121 CGCACCCGTAGACCAGACCCCGAGGACCCATGGGCCAGAGAGCATTACCTTC 180 181	661 GAGTOGGACCTGGACCTGCCCGGAATGGCCCCCTGTCTCCATGTCCGACCGA

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Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
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1. .140207
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Direct Submission
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                   CGCACCCGTAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC
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                                                            ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCCACCTGCTGCTCTGGCGACCC
                                                                                 ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCCACCTGCTGCTCTGGCTCTGGCGACCC
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AL356390

Human DNA sequence from clone RPI1-344H11 on chromosome 1 Contains the NROB2 gene for nuclear receptor subfamily 0 (group B, member 2), the 5' end of a novel gene (FLJ12455), the NUDC gene fornuclear distribution gene C homolog (A. nidulans), a novel gene (FLJ34633), a ribosomal protein L12 (RPL12) pseudogene, a ribosomal protein L12 (RPL12) pseudogene, a ribosomal protein L32 (RPL32) pseudogene, a novel gene (FLJ34633), a nov CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromesome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group, Further information, can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ries sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a MAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
1. (bases 1 to 140207)
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/note="Sequence from overlapping clone RP4-633N17
(Al.137860). Assembly confirmed by restriction digest.
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HTG; DC2; FLJ12455; FLJ34633; NROB2; NUDC; RPL12; RPL32
Homo sapiens (human)
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RP11-344H11 is from the library RPCI-11.2 of
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute
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HEBDLDLPBRGGSGNSSRAS BIDVLI FRKLTFELFSVHQIDELAKCTSDYPYLEKKTSKIS
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HETMVGSGLSQDELTVQISQETTADAIARKLRPYGAPGYPASHDSSFQGTDTDSSGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MPRPGHPRPASGPPRLGPWERPTELCLETYDKPPQPPPSRRTRR
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GACVRGCSPCLSTEDSTEGTAEANWAKEHNGVPPSPDRAPPSRRDGQRLKSTMGSSFS
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91374. .91568 91563. .91779,92631. .92686,92779. .92982,
110273. .110356,112510. .112713))
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Tr:Q862X1 Tr:Q8AVWO Tr:Q8C2KO Tr:Q90YV6 Tr:Q9NQ02"
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                                                                                                                                                         'product="ribosomal protein L12 (RPL12) pseudogene"
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/note="Sequence from uni-directional dGTP big dye
terminator reads only."
join (82059. 831097, 83683. 83757, 84288. 84370)
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79656. __79827
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/product="nuclear distribution gene C homolog
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|standard_name="OTTHUMP00000004472"
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/db_xref="G1:55959149"
/db_xref="UniProt/TrEMBL:Q5QP32"
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gene="RP11-344H11.3"
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GLLKYCHLLVRGFRPRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGAD
AARRYACLVTLHRVVNESTVCLMMHERRQTLDLIAALALQALAEGGFAATAALAWRPP
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GRHLSGLSWPQVKRLDALLSBPIPIHGRGNFPTLSVQPRQIVQVVRSTLEEQGLHVHS
VRLHGSAASHVLHPESGLGYKDLDLVPRVDLRSEASFQLTKAVVLACLLDFLPAGVSR
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/locus tag="RP11-344H11.5-001"
/note="match: proteins: Sw:094008 Sw:P02433 Sw:P17932
/note="match: proteins: Sw:094006 Sr:BAC21646 Tr:BAC25812
Tr:CAD98375 Tr:C660373 Tr:Q22280 Tr:Q86JP7 Tr:Q86QS0
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                                                                                                                                                                                                                               /product="novel protein"
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Em:BC012790.2 Em:BC014160.1 Em:BC014160.2 Em:BC038001.1"
join(21772. 22032, 27482. .28495)
/gene="RP11-344H11.8"
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Em:BM021923.1 Em:BM682682.1 Em:BQ646324.1 Em:BQ892187.1
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/note="match: proteins: Tr:AAH54857 Tr:BAB28595
Tr:EAA12661 Tr:Q72WJ3 Tr:Q8TBU1 Tr:Q9CP22 Tr:Q9NRP0
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complement (join(53464. .53610,53925. .54274))
/locus_tag="RPl1-344H11.4-001"
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/locus_tag="RP11-344H11.8-001"
complement(join(33541.7-601"
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complement(join(33541.34H11.7-001"
/locus_tag="RP11-344H11.7-001"
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complement(join(53464. .53610,53925. .54274))
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| 2010/12[60]. 220322,27482. .29419|
| Gene="RP11-344H11.8"
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29398. .29403
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/db_xref="UniProt/TrEMBL:Q96A09"
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complement (50415. .50811)
/locus_tag="RP11-344H11.5-001"
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Macina,R.A., Recipon,H., Chen,S.Y., Sun,Y. and Liu,C.
Compositions and methods relating to lung specific genes
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                                                French: WO 02068633-A 56 06-SEP-2002;
Diadexus, Inc. (US)
Location/Qualifiers
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Pred. No. 0;
0; Mismatches
                                                                                  1. .1977
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.9%;
Matches 1103; Conservative
Hominidae; Homo
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                     ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTCTGGCGACCC
                                                               TGGGTGTGGGGAGTGGTGCCTGCCTTCTGCTTCCGCCGCCGCGGGATTGCCTCCAG
                                                                                                                                                                                                                                                                                  GCCCCTGATGCGGACTCCTGCTGCAAGAGCACCACTGGCCGATCCCCCACCATGCGACAC
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                                                     TGGGTGTGGGGAGTGGTGCCGGGCTGCCTTCTGCCTCCGCCGCTGCCGGGATTGCCTCCAG
                                                                                               CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG
                                                                                                           GCACCCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC
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          AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT
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1161 CGGCATCATTGGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGTCG 1220		SULT 9 592304 CUS CUS TENITION Homo sapiens chromosome 1 clocasion ALS92304 ALS92304. GI:14586390 WWORDS HTG; HTGS PHASEL; HTGS CANCEL HOMO sapiens (human) SUGANISM Homo sapiens (human) Mammalia; Eutheria; Buarchont Hominidae; Homo. AUTHORS JOURNAL Submitted (24-UUL-2001) Sange CB10 1SA, UK. E-mail enquirie
GGGAGTGAAC 1496	PAT 22-NOV-2002 Euteleostomi; rrhini; enes and i, Gaps 1; crarrcrrrc 657	CCGAGAATT 717 CCGAGAAATT 717 CCGAGAAATT 980 CCGAGAAATT 980 CCGATGAGCT 776 CCGATGAGCT 1040 CCGACCTTAT 1100 GCGACCTTAT 1100 GCCTGGTACG 896 GCTGGTACG 896 GCTGGTACG 1160 CCGAGGGTCG 956 CCGGAGGGTCG 956
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8 6 8 6 8 6 8 6	AK535090 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL FRATURES SOURCE AUTHORS TITLE JOURNAL PRATURES SOURCE SOURCE ORGIN ORIGIN OUELY MA BEST LOC MATCHES	4 8 4 8 4 8 4 8

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96686 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGGC
                         54.7%;
                                                      Conservative
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Matches 1037; Conserv
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                                                                                           Assembly program: XGAP4; version 4.5 Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Sequencing vector: plasmid; L08752; 100% of reads Consensus quality: 110287 bases at least Q40 Consensus quality: 110500 bases at least Q30 Consensus quality: 110681 bases at least Q20 Insert size: 111138; sum-of-contigs of the contigs of the contage: 11.23x in Q20 bases; sum-of-contigs quality coverage: 11.23x in Q20 bases; sum-of-contigs quality
                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. On the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                     18958: contig of 18058 bp in length
1859 35144: contig of 16986 bp in length
1853 35244: gap of 100 bp
1855 35444: gap of 100 bp
1855 354710: contig of 19466 bp in length
1711 54810: gap of 100 bp
1811 72936: contig of 18126 bp in length
1812 92888: contig of 18852 bp in length
1813 92888: contig of 19852 bp in length
1819 92888: gap of 100 bp
1889 108739: contig of 15751 bp in length
1840 111738: contig of 2899 bp in length
1840 111738: contig of 2899 bp in length
1850 108439: gap of 100 bp
1864 111738: contig of 2899 bp in length
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fragment chain:I
clone_end:17
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fragment_chain:2"
108840. _111738
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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  Length 111738;
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    DB 14;
Score 937; DB
Pred. No. 0;
0; Mismatches
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT 10 AX535028

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REFERENCE AUTHORS TITLE

JOURNAL FEATURES

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1263 ACCAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCCTG 1322
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot., D., Lamson, G., Dramarc, R., Crkenjakov, R., Drmanac, S., Dickson, M., Labat, J., Leshkowitis, D., Kita, D., Garcia, V. and Strache-Crain, B. Human genes and gene expression products Patent: WO 010258-A 177 11-JAN-2001; CHIRON CORPORATION (9); HYSEQ, INC. (US)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                              Salceda,S., Macina,R.A., Recipon,H., Pluta,J., Sun,Y. and Liu,C. Compositions and methods relating to breast specific genes and proteins
                                                                                                                                                                                                                                                                                                                                                                                                             1203 GCCAGGCCCAGCTGCCACACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGGGG
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                                                                                                                                                               Diadexus, Inc. (US)
Location/Qualifiers
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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100.0%; Pred. No. 1.5e-211;
ive 0; Mismatches 0;
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Diadexus, Inc. (US)
Location/Qualifiers
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Sequence 104 from Patent W002077232.
AX644346.1 GI:28610405
                                                                                                                                                      AX535028 385 bp 1
Sequence 55 from Patent WO02068633.
AX535028
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                        96746 TCAGGTCTCAGCCAGGATG 96764
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Matches 385; Conservative
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RADOMIC, TERVENJAKOV, MARK DICKSON, SNEZANA DRMANAC, IVAN LABAT,
DENA LESHKOWITZ, DAVID KITA, VERONICA GARCIA, LEE WILLIAM JONES,
BIRJIT STACHE CRAIN
C12N15/09, C12N15/09, C07K14/47, C07K14/82, C07K16/18, C12N1/15, PC
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1 (bases 1 to 300)

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C., Giese, K., Randaazo, F., Kennedy, G.C., Pot, D., Kannaac, R., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M., and Crain, B.S.
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140 CGCCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC 199
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                                                                                       200 CGCACCCGTAGACCCGAGGACCCTGGCCACCATGGGCCAGAGAGATTACCTTC
                                                                                                                                                                                                    241 TGGGTGTGGGAGTGGCGGGCTGCCTTCTGCTTCGCCGGGGATTGCCTCCAG
                                                       181 ATCTCTGGCTCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTCTGGCGACCC
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/db_xref="taxon:9606"

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JP 2002519000-A/861.
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Homo sapiens
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Patent: WO 0102568-A 2132 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
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                                                                                                                                                                                                                                                     805 CTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTG
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                                                                                                                                   19.5%; Score 334; DB 6; Length 393; 100.0%; Pred. No. 7.38-182; ive 0; Mismatches 0; Indels
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    /note="n = A,T,C or G"

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db_xref="taxon:9606"
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Matches 321; Conservative
                                                                                                                                                                   Best Local Similarity 100.
Matches 334; Conservative
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                                                                                                                                            Query Match
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/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                            Best Local Similarity 99.7
Matches 299; Conservative
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DD 08-ANA-2002
PF 22-DEC-1999 US 60/068755,03-APR-1998 US 60/080664 PR
21-OCT-1998 US 60/068755,03-APR-1998 US 60/105877 PR
21-DEC-1998 US 60/105234,27-OCT-1998 US 60/105877 PR
21-DEC-1998 US 60/105877 PR
21-DEC-1998 US 60/105877 PR
21-DEC-1998 US 60/105877 PR
21-DEMINGUEZ GARCIA, FLINGER, CHRISTOPH REINHARD, KLAUS GIESE, FILIPPO PI RANDAZZO,
PI GIULIA C KENNEDY, DAVID POT, ALTAF KASSAM, GEORGE LAMSCOT,
PI RADOMIR CRKVENJAKOV, MARK DICKSON """
PI BENA LESSIKOMITZ, DAVID """
PI BENA LESSIKOMITZ, DAVID """
PE BIRGIT STACHE ""
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1 (bases 1 to 300)
Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C., Giese, K., Randazzo, P., Kennedy, G.C., Pot, D., Drmanac, R., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M., Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V., Jones, L.W. and Crain, B.S.
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                                                                                                                                                                                                                                       CTCGGAGGGTCGTTCAACTCGGGCTGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCA 1004
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                      CTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGG
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                                                   CTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGGATGCTGAGGG
                                                                                                                                          CCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGAC
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    Indels
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Key Location/Qualifiers
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    0; Mismatches
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/organism="Homo sapiens"
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C1201/68,C12N15/00,
PC C12N5/00,C12N15/00
CC Human gene and gene FFH Key Local
FFH Key Local
FT Source 1...
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JP 2002500010-A/34.
Homo sapiens (human)
Homo sapiens
    Conservative
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                                                                                                        740 TGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCCAAGTGCACATCAGACACTG 799
                                                                                                                                                                                                                859
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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60 GGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTATCTTAACATGACCACAGTTTGTAAGT
                                                                                                                                            1 TGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCCAAGTGCACATCAGACACTG
                                                                                                                                                                                                                TGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACC
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  Length 300;
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BD216745.1 GI:33026515
JP 2002519000-A/4887.
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                                                    Indels
14.5%; Score 249; DB 6; I
99.7%; Pred. No. 2.2e-132;
iive 0; Mismatches 1;
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Sequence 116 from Patent WO02068633.
AXS35089
AXS35089.1 GI:25261786
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramon, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.W., Butterfield, Y.S., Krzywinski, M. I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="MGGC:11921 InAGE:3599314"
/tissue type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal Tarcinoma. 5 month old virgin mouse."
/clone lib="NCI CGAP_Mam6"
/lab_host="DH108"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="MGI:1916323"
/translation="MSAPSAPHRAVAPGGQTLRTLATMGQRVSPSFQALQNQPTSPQPA
ASSGAPGYGFGGESSASARAGACSAVGLVCGAAAPAYLPETPLKGLPKPPGFRNTM
ASSGAPGYGFGGLPSSASARAGACSAVGLVCGAAAPAYLPETPLKGLPKPPGFRNTM
VCPPARTVHPPAAGMARGSRPAMAAASATLMLSSKASLSTPTAMPPPGSLTWTPAARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 16 Row: p Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19526881. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWPSILPHGTACLAPSPTAPAALRSTTPSMNRTWTCLRWAVAPCRAGRSTCLFSRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submitssion
Submitted (27-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing Destrict College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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/product="RIKEN cDNA 1810019J16"
/protein_id="AAH06890.1"
/db_xref="G1:13905190"
/db_xref="G1:13905190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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/gene="1810019J16Rik"
/db_xref="GeneID:69073"
/db_xref="MGI:1916323"
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/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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TITLE
JOURNAL
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Mus musculus RIKEN cDNA 1810019J16 gene, mRNA (cDNA clone MGC:11921
IMAGE:3599314), complete cds.
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                                                                                                                                                              Hominidae; Homo.

I (Dasea 1 to 728)

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C., Giese, K., Randazzo, F., Kennedy, G.C., Pot, D., Drassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M., Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V., Jones, L.W. and Crain, B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JULIE SUDDUTH KLINGER, CHRISTOPH REINHARD, KLAUSE GIESE, FILIPPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRMANAC,
RADOMIR CRKVENJAKOV, WARK DICKSON, SNEZANA DEWANAC, IVAN LABAT,
DENA LESHKOWITZ, DAVID KITA, VERONICA GARCIA, LEE WILLIAM JONES,
BIRJIT STACHE CRAIN
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIULIA C KENNEDY, DAVID POT, ALTAF KASSAM, GEORGE LAMSON, RADOJE
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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60/080515 PR
60/105234 PR
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100.0%; Pred. No. 1.6e-09;
ive 0; Mismatches 0; Indels
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Patent: JP 20025;9000-A 4887 02-JUL-2002;
CHIRON CORP, HYSEQ INC
OS HOMEO Sapiens (human)
PN JP 2002519000-A/4887
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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GapB

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Indels

100.0%; Pred. No. 1.8e-09; ive 0; Mismatches 0;

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Conservative
Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                                                                          DEFINITION
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AUTHORS
TITLE
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an allernate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VECTOR: pBACe3.6 Sequencing Consortium whole genome Sequencing Consortium whole genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has
                                                            ö
                                                                                                                                                                                                                                                                                                          AL627228 193813 bp DNA linear ROD 04-FEB-2003
Mouse DNA sequence from clone RP23-137L22 on chromosome 4, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (04-FEB-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 4, 2003 this sequence version replaced gi:22474404.
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the clone being a YAC. RP23-137L22 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                            ö
     Length 1680;
                                                            0; Indels
                                                                                                                                             885 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 922
                                                                                                                835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 872
  Query Match
2.2%; Score 38; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a phred quality of at least 30.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP23-137L22"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                       AL627228.31 GI:28208155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 193813)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hopkins, B.
                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                        RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                  AL627228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
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2.2%; Score 38; DB 9; Length 193813;

Query Match

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Schusghardh; murchaes; murines; Karlus.

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwant, F.J.,
McKernan, K.J., Male, M.S., Stancher, P.H., Hulyk, S.W.,
Villalon, D.K., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Bouffard, G.G., Blakesley, R.W., Touchman, A., Rodrigues, S.,
Butterfield, Y.S., Krzywinsk, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinsk, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: d Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Express Genomics
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Wheb site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                    BC079148 1718 bp mRNA linear ROD 15-SEP-2004 Rattus norvegicus similar to hypothetical protein FLJ34633, mRNA (cDNA clone MGC:94165 IMAGE:7128510), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (02-A02-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Bute
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                          104723 ATCAGCACCATCACGCAGGACTACCACCTGGATGAGCA 104760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC079148.1 GI:50927712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Director MGC Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 1718)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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1 (bases it collection) "Albamaton, S., Adams, C., Alder, J.,
Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,
Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barantead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Davila, M.L., Davis, C., Dary-Carroll, L., De Anda, C., Dederich, D.,
Draper, H., Dugan-Rocha, S., Deramo, C., Ding, Y., Dinh, H., Dirya, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Pan, G.,
Fraser, C.M., Gabisi, A., Gante, R., Garria, M., Guevra, W.,
Gebregeorgis, B., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M.,
Gebregeorgis, B., Geer, K., Gill, R., Gracia, A., Hogues, M.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Harvey, Y., Havlak, P., Hawes, A., Honderson, N., Hernandez, J.,
Jackson, L., Jacob, L., Jiang, H., Levan, J., Idlebird, D., Jackson, A.,
Karpathy, S., Kelly, S., Kally, S., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACU95979 235419 bp DNA linear HTG 09-NOV-2002
Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACVRSCSPCLSAGDPIEGSSEAAWAKEHNGVPPSPDRAPPSRRDGGKLKTSMGSSFS
YPDVKLKGIPVYPYRHATSPVPDADSCCKEPLADPPPTRHSLPSTFTSSPRGSEEYYS
FHESDLDLPEMGSGSMSSREIDVLIFKKLTELFSVHQIDELAKCTSDTVFLEKTSKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLISSITQOYHLDEQDAEGRLVRGIIRISTRKSRSRPQTSEGRSARSTRAAADSGH
ETWYGSGLSQDELIVQISQETTADAIARKLRPYGAPGYPASQDSSFQGTDISSGAPL
LQVYC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MPRPGQPRPSSGPPRLGPWERPTELCLETNDERSQPPPGRRTRR
PDPKDPGHHGPESITFISGSAEPANEPPTCCLLWRPWGWDWCRAAFCFRRCRDCLQRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus
1 (bases 1 to 235419)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                product="similar to hypothetical protein FLJ34633"
    protein id="AAH79148.1"
    db_xref="G1:50927713"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.7%; Score 29; DB 9; Length 1718;
100.0%; Pred. No. 0.00028;
ive 0; Mismatches 0; Indels
                  /clone="MGC:94165 IMAGE:7128510"
/tissue type="Kidney, rat (Brown Norway)"
/clone lib="NIH MGC_236"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1063 GACAGTGGCCATGAGACCATGGTGGCTC 1091
                                                                                                                                                                           'note="Vector: pExpress1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GeneID:313018"
                                                                                                                                                                                                                                                                      db_xref="GeneID:313018"
db xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                  dene="MGC94165"
                                                                                                                                                                                                                                            gene="MGC94165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC095979.7 GI:24818145
                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC095979
                                                                                                                                                                                                                                                                                                                 CDS
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COMMENT

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On Nov 9, 2002 this sequence version replaced gi:22772470.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads will be indicated in the feature table.
Litu,J., Litu,W., Litu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Mahcshwari,M., Mahindartne,M., Mahloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Manhiney,S., McLeod,M.P., Moneill,T.Z., Menen,E.,
Manhiney,S., McLeod,M.P., Moneill,T.Z., Menen,B.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Fennncoch,C.,
Plopper,F., Poindexter,A., Perez,L., Fennncoch,C.,
Plopper,F., Poindexter,A., Perez,L., Frannsch,C.,
Ratilly,B., Railly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rachlin,E., Reeves,K., Regier,M.A., Railly,B., Railly,M., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tablor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Ver,J., Warren,R., Wei,J., Wanler,F.,
Williams,G., Wallson,R., Walch,X., Wen,J., Yoon,U.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R.,
Nhick, Shhissin,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley,K.C.
Direct Submission
Submitted (17-SRP-2001) Human Genome Sequencing Center, Department
Submitted (17-SRP-2001) Human Genome Sequencing Center, Department
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235419)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project Information
Center project name: GEBU
Center clone name: CH230-11020
Center clone name: CH230-11020
------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 227458 bases at least Q40
Consensus quality: 228649 bases at least Q30
Consensus quality: 228649 bases at least Q20
Estimated insert size: 235033; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
2 (bases 1 to 235419)
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Sciurognathi; Murcidea; Murinae; Rattus.

1 (bases 1 to 249406)

Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Anguiano, D., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Anlen, C., Allen, H., Abyagi, A., Ayodeji, M., Baca, E., Baden, H. Baldaranaike, D., Barber, M., Barnstead, M., Benamed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bulay, C., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, M. D., Devia, C., Coyfe, M., Cree, A., Disoura, L., Davia, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Ban, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flaggi, N., Forbes, L., Foster, M., Gabisi, A., Ganta, R., Gardy, M., Garer, M., Guerra, W., Guerra, W., Guerra, W., Guerra, W., Gunararne, P., Haaland, W., Hanli, C., Hamilton, C., Harilton, C., Harvey, Y., K., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
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Rattus norvegicus clone CH230-180E4, WORKING DRAFT SEQUENCE.
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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100.0%; Pred. No. 0.00031;
ive 0; Mismatches 0; Indels 0;
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AC118963.4 GI:25009106
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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1.7%; Score 29; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 29; Conservative 0; Mismatches
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228652. .228751
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site:EcoRI
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219911. .220573
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ALL SUBMILTERIOR (15-NOV-2002) Human Genome Sequencing Center, Department of Wolecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23269749.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Jackson, A., Jackson, E., Johnson, R., Liu, Y., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, M., Liu, Y., London, P., Longacre, S., Loyez, J., Liu, M., Mahindartne, M., Mahindar, M., Martin, R., Martinez, B., Mapua, P., Martin, K., Martin, R., Martinez, B., Mapua, P., Martin, K., Martin, R., Martinez, B., Malosay, J., Morris, S., Munidasa, M., Murphy, M., Nair, L., Naveon, J., Newton, N., Nguyen, N., Norris, S., Paul, H., Perez, A., Perez, L., Pfanhcoch, C., Paloper, F., Poindexter, A., Perez, L., Pfanhcoch, C., Pluzco, M., Quiroz, J., Rachlin, B., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutcon, A., Svatek, A., Tabor, P., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walter, R., Weis, X., White, F., Wang, J., Warren, J., Warren, R., Weis, X., White, F., Wang, J., Zhao, S., Dunn, D., Von, U., Yu, F., Zhang, J., Zhao, S., Dunn, D., von Niederhausern, A., Weise, R., Pur, Shuith, D. R., Shuith,
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Unpublished
Voleses 1 to 249406)
Voleses 1 to 249406)
Direct Submission
Submitted (12.APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Neaes 1 to 249406)
Rat Genome Sequencing Consortium.
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Consensus quality: 213357 bases at least Q40
Consensus quality: 215358 bases at least Q30
Consensus quality: 217213 bases at least Q20
Estimated insert size: 223109; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-180E4
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai, Bucheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

Sciurognathi; Muridae; Muridae; Murinae; Rattus.

I (bases I to 256017)

Sciurognathi; Muridae; Murinae; Rattus.

I (bases I to 256017)

Suran, D.M., Adana, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Burdaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Burder, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavaz, D., Chavaz, D., Chen, G., Chen, Z., Chon, Z., Chocko, J., Chavaz, D., Chavaz, D., Chen, Z., Chen, Z., Chou, M.D., Dathorne, S.R., David, R., Davis, C., Coy, C., Chan, S., Durbin, K.J., Delaney, K.R., Deladaó, C., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Davis, C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Harris, C., Harris, K., Harris, K., Harris, C., Harris, K., Lude, S., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Lou, K., Ludiar, M., Martina, R., Martina, M., Morgan, M., Morgan, M., Morgan, M., Morgan, M., Morgan, M., Nguyen, 
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Rattus norvegicus clone CH230-1B9, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
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100.0%; Pred. No. 0.00031;
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                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/organism="Rattus norvegicus"
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Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:23267435.

The sequence in this assembly is a combination of BAC based reads and whole genome shocyun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat//f. Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                       Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rodas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Gisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutch, A., Svatek, A., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Willams, G., Walliamson, A., Willalon, D., Vinson, R., Wang, Q., Williams, G., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley,K.C.
Direct Submission
Submitsed (05-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 256017)
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Assembly program: Phrap, version 0.990329
Consensus quality: 214627 bases at least Q40
Consensus quality: 219116 bases at least Q30
Consensus quality: 219116 bases at least Q30
Consensus quality: 221911 bases at least Q30
Estimated insert size: 2221941; aum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 83721: contig of 83721 bp in length
22 83821: gap of unknown length
52 253567: contig of 169746 bp in length
58 253667: gap of unknown length
68 256017: contig of 2350 bp in length.
Location/Qualifiers
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-1B9
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PAT 06-AUG-2001
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                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
assessment, prevention, and therapy of cervical cancer
Patent: WO 014467-A J. 14 JUN 2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Millennium Predictive Medicine, Inc.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therappy of cervical cancer
Patent: WO 0143467-A 1200 14-JUN-2001,
Millennium Predictive Medicine, Inc. (US)
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100.0%; Pred. No. 0.001;
tive 0; Mismatches 0; Indels
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organism="Rattus norvegicus"
mol_type="genomic DNA"
db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                      /estimated length=unknown 83822. .85574 /note="wgs_contig" 219978. .221353
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/organism="Homo sapiens"
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                                                 /clone="CH230-1B9"
6668. .7475
/note="clone_boundary
clone_end:T7
                                                                                                                                          end sequence:BH274997"
38358. .39527
/note="wgs_contig"
67950. .69005
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253568. .253667
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8781. .81213
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3722. .83821
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Best Local Similarity 100.0%
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Novel genes, compositions, kits, and methods for identification,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                          Schlegel, R., Deeds, J., Berger, A. and Zhao, X. Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer Patent: WO 0142467-A 1358 14-JUN-2001, Millennium Predictive Medicine, Inc. (US)
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100.0%; Pred. No. 0.015;
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/db_xref="taxon:9606"
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CQ424843.1 GI:41377072
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Genes differentially expressed in human prostate cancer and their
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelec
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 9877 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                          Score 26; DB 6;
Pred. No. 0.015;
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Sequence 17410 from Patent WO0170979.
CQ410339
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Sequence 37484 from Patent WO0160860.
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                                                                                1. .576
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    255
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Query Match

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KEYWORDS SOURCE ORGANISM

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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therappy of breast cancer
Patent: WO 0151628-A 6873 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification,
Genes, compositions, and therapy of ovarian cancer
Basessement, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 11387 27-8EP-2001;
Millennium Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 0.057;
tive 0; Mismatches 0; Indels
    Length 310;
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Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 25; Conservative 0; Mismatches 0; Indels
  1.5%; Score 25; DB 6; Le
llarity 100.0%; Pred. No. 0.057;
Conservative 0; Mismatches 0;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Genes differentially expressed in human prostate cancer and their
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 017097-A 5095 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Sequence 5095 from Patent WO0170979.
CQ398024
                                                                                                                                                                                                                                                                                                                                      304 bp Di
Sequence 7524 from Patent WO0160860.
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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CQ475657.1 GI:41441276
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Best Local Similarity 100.03
Matches 25; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                      Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 150;
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Immune-related proteins and the regulation of the Patent: WO 031002599.A 15 09-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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Berka,R., Bashkirova,E. and Rey,M.
Methods for monitoring multiple gene expression
Patent: WO 2005030998-A 1051 07-APR-2005;
Novozymes Biotech, Inc. (US)
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100.0%; Pred. No. 0.22;
iive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches
          Sequence 1051 from Patent WO2005030998.
CS067068
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Sequence 17222 from Patent WO0170979.
CQ410151 GI:41317932
                                                                                                                                                                                                                                                                                                                                                    /organism="Hypocrea jecorina"
/mol_type="unassigned DNA"
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Sequence 15 from Patent WO03002599.
AX718965
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/mol_type="unassigned DNA"
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                                                                           CS067068.1 GI:62819876
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Best Local Similarity 100.0
Matches 24; Conservative
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AX718965
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                                                                                                                          PAT 06-AUG-2001
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 0142467-A 985 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 0.058;
tive 0; Mismatches 0; Indels
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    .463
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                                                                                                                        AX185290 359 bp 1
Sequence 985 from Patent WO0142467.
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GTAAGTACCTCGGCGCGCGACCACGC
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Best Local Similarity 100.
Matches 25; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 11632 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Pacent: WO 0770979-A 16395 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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                                                                                                                                                                                                                                                Length 274;
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                                                                                                                                                       /mol_type="unassigned DNA" /db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 17222 27-5EP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 534S 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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1.4%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches
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                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db xref="taxon:9606"
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/organism="Homo sapiens"
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                                             Hominidae; Homo.
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DEFINITION ACCESSION VERSION

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS

TITLE

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FEATURES

ORIGIN

RESULT 41 CQ398274/c

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PAT 23-JAN-2004

SOURCE

AUTHORS REFERENCE

ACCESSION VERSION KEYWORDS

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PAT 23-JAN-2004
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therappy of ovarian cancer
Patent: WO (170979-A 10381 27-28D-2001;
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee, J. and Lillie, J. Genes, compositions, kits, and method for identification, dessessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 2976 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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1.4%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches
               1.4%; Score 24; DB 6;
100.0%; Pred. No. 0.22;
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100.0%; Pred. No. 0.22;
vative 0; Mismatches
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Sequence 10381 from Patent W00170979.
CQ403310. GI:41311091
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0
Matches 24; Conservative
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Matches 24; Conservative
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CQ403310/c
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CQ395905/c
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ACCESSION
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: W 0 0170979-A 9991 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Genes, compositions, kits, and method for identification,
Genes, compositions, kits, and therapy of ovarian cancer
Basesement, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 4074 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 9991 from Patent WO0170979.
CQ402920
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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CQ397003/c
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 5545 19-JUL-2001,
Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
assessment WO 14467-A 929 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 0.22;
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Sequence 5545 from Patent WO0151628.
CQ420511
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                                   AX185234 331 bp 1
Sequence 929 from Patent WO0142467.
                                                                                                                                                                                                                                                                                                                                                                               /mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .337
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/organism="Homo sapiens"
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                                                                                        AX185234.1 GI:15136619
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer passessment, NO 0170979-A 9305 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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llarity 100.0%; Pred. No. 0.22;
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Sequence 17947 from Patent WO0170979.
CQ410876
                                                                                                                    Sequence 9305 from Patent WO0170979. CQ402234
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                   Lee, J. and Lillie, J.

Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 4711 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
| J. 368 | /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"
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tive 0; Mismatches
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CQ398887
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes differentially expressed in human prostate cancer and their
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                               Schlegel, R., Deeds, J., Berger, A. and Zhao, X. Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer Patent: WO 014467-A 982 14-JUN-2001; Millennium Predictive Medicine, Inc. (US)
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100.0%; Pred. No. 0.22;
iive 0; Mismatches 0; Indels
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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    .346
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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 GI:15136675
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CQ397640/c
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 017097-A 12238 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 5958 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           Sequence 12238 from Patent WO0170979.
CQ405167
                                                                                                                                                          Query Match

1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.2
Matches 24; Conservative 0; Mismatches

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therappy of ovarian cancer
Patent: WO 017099-A 15765 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 2902 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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1.4%; Score 24; DB 6; Length 376;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels
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Sequence 16765 from Patent W00170979.
CQ409694
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Sequence 2902 from Patent WO0170979.
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/organism="Homo sapiens"
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/db xref="taxon:9606"

    .391
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CQ409694.1 GI:41317475
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CQ395831.1 GI:41303612
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: W O 0170979-A 3267 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers
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1.4%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches
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CQ402521
CQ402521.1 GI:41310302
                                                                                                                       392 bp Dr
Sequence 3267 from Patent WO0170979.
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/db xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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         110 TAAGTACCTCGGCCGCGACCACGC 87
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CQ396196/c
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CQ402521/c
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 9231 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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1.4%; Score 24; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels
           Score 24; DB 6; Length 391;
Pred. No. 0.22;
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100.0%; Pred. No. 0.22;
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1.4%; Scc. 100.0%; Pred. No. c. 0; Mismatches
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Sequence 9231 from Patent W00170979.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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     Query Match
Best Local Similarity 100.
Matches 24, Conservative
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CQ409304/c
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RESULT 66

1690 TAAGTACCTCGGCCGCGACCACGC 1713

CQ476176/c

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                       Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 17159 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Genes, compositions, kits, and method for identification, assessment, prevention, and therappy of ovarian cancer Patent: WO 0170979-A 5221 27-5EP-2001;
Millennium Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 0.22;
live 0; Mismatches
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100.0%; Pred. No. 0.22;
iive 0; Mismatches
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CQ404437
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                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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CQ398150.1 GI:41305931
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                       sapiens (human)
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CQ398150/c
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                           Schlegel, R., Endege, W.O. and Monahan, J.E.
Genes differentially expressed in human prostate cancer and their
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 16049 27-SEP-2001, Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                       linear
                                                                                                                                                                                                                                                                                                       Patent: WO 0160860-A 8043 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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            404 bp Dl
Sequence 8043 from Patent WO0160860.
CQ476176
CQ476176.1 GI:41441795
                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="unassigned DNA" /db_xref="taxon:9606"
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Homo sapiens
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                                                                                                                                            Homo sapiens
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RESULT 67 CQ408978/c

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

REFERENCE

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FEATURES

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/organism="Homo sapiens"
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Homo sapiens
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nes 24; Conserv
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CQ507382/c
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JOURNAL
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                        Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
Basesement, prevention, and therappy of ovarian cancer
Patent: WO 0170979-A 11508 27-SEP-2001,
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 12779 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 0.22;
ive 0; Mismatches 0; Indels
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Sequence 15689 from Patent WO0170979.
CQ408618 GI:41316399
                                                                                                                                                                                                                                                                                                                                                                                        CQ405708 420 bp DNA Sequence 12779 from Patent WO0170979.
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/db_xref="taxon:9606"
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Hominidae, Homo
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Matches 24; Conserva
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Genes differentially expressed in human prostate cancer and their
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 1710979-A 5813 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
Patent: WO 0170979-A 15689 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 0.22;
:ive 0; Mismatches (
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100.0%; Pred. No. 0.22;
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Sequence 39249 from Patent WO0160860.
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Sequence 5813 from Patent WO0170979.
                                                                                  1. .420
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CQ507382.1 GI:41473592
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes differentially expressed in human prostate cancer and their
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                             CQ411551 432 bp DNA Sequence 18622 from Patent WO0170979. CQ411551
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1.4%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches
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CQ506077
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1.4%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches
Best Local Similarity 100.0%; Pred. No. 0.22; Matches 24; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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CQ411551/c
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Genes differentially expressed in human prostate cancer and their
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 18496 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                                                                                 DB 6; Length 424;
0.22;
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                       426 bp DNA Sequence 18496 from Patent W00170979. CQ411425. G1:41319206
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.2
Matches 24; Conservative 0; Mismatches
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/db_xref="taxon:9606"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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CQ474699/c LOCUS

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PAT 23-JAN-2004

CQ396029/c

RESULT 79

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REFERENCE

TITLE

VERSION KEYWORDS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and method for identification, assessment, prevention, and therappy of ovarian cancer Patent: WO 0170979-A 15845 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                         Lee,J. and Lillie,J.

Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 18016 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 0.22;
tive 0; Mismatches
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Sequence 15845 from Patent WO0170979.
CQ408774
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DNA
           Sequence 18016 from Patent W00170979.
CQ410945
CQ410945.1 GI:41318726

    .442
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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442 bp
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Best Local Similarity
CQ410945
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CQ397235/c
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                      Lee,J. and Lillie,J.
Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 017097-A 3100 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 0.22;
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                                                                                     437 bp DN Sequence 3100 from Patent WO0170979. CQ396029
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56 TAAGTACCTCGGCCGCGACCACGC 33
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CQ402355.1 GI:41310136
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24; Conservative
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Best Local Similarity
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CQ402355/c DEFINITION

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RESULT 81 CQ410945/c

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Patent: WO 0160860-A 45120 23-AUG-2001;
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                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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                                                                                    Lee,J. and Lillie,J.
Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 4306 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 10610 27-SEP-2001,
Millennium Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 0.22;
tive 0; Mismatches 0; Indels
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CQ504192
CQ504192.1 GI:41470221
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                                                                                                                                                                                                                      /mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .446
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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CQ403539.1 GI:41311320
Homo sapiens (human)
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Best Local Similarity 100.
Matches 24; Conservative
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Genes differentially expressed in human prostate cancer and their
Schlegel, R., Endege, W.O. and Monahan, J.E.
Genes differentially expressed in human prostate cancer and their
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Genes differentially expressed in human prostate cancer and their
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                                                                           Patent: WO 0160860-A 36059 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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0.22;
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100.0%; Pred. No. 0.22;
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CQ506124
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    .446
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Sequence 18705 from Patent WO0170979.
CQ411634
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LOCUS CQ396273 464 bp DN
DEFINITION Sequence 3344 from Patent W00170979.
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Sequence 66 from Patent WO02064788.
AX523478
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/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                                    ACCESSION
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                                 RESULT 89
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|protein id="CACO4516.1"
|db_xref="G1:990727"
|db_xref="G0:909727"
|db_xref="G0:Q9F433"
|db_xref="UniProt/TrENBL:Q9F433"
|cdb_xref="UniProt/TrENBL:Q9F433"
|cdb_xref="UniProtVLINRYPLESIAIRTLLENKGVSVTGEAINGWDALRIVDQLOGNITIVDVDLDDIDGIGLVETLERRALYGSIIVTSNKYLGRDHARGSSRVDLQA"
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Submitted (22-AUG-2000) Yang S., Life Science, National Tsing Hua
University, 101, Section 2 Kuang Fu Road, Hsinchu, 300, TAIWAN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ293850.1 GI:9909726
EVGA gene; positive transcription regulator EVGA.
Klebsiella pneumoniae
Klebsiella pneumoniae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lai, Y.C., Yang, S.L., Peng, H.L. and Chang, H.Y.
Identification of genes present specifically in a virulent strain of Klebsiella pneumoniae
Infect. Immun. 68 (12), 7149-7151 (2000)
                                                                                                                                                                                                                                                                      Gaps
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ive 0; Mismatches 0; Indels
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tive 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
/strain="CG43"
Millennium Predictive Medicine, Inc. (US)

    .446
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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contig region pSL042"
complement(26. .322)
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/codon_start=1
/trans1_table=11
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/country="Taiwan"
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PAT 23-JAN-2004

ACCESSION VERSION KEYWORDS

ORGANISM

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FEATURES

REFERENCE AUTHORS

TITLE

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                Lee, J. and Lillie, J.

Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 15851 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 4472 27-SEP-2001,
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                   Length 471;
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100.0%; Pred. No. 0.22;
:ive 0; Mismatches
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1.4%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches
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Sequence 4472 from Patent WO0170979.
                                                                                                                                                                                                          1. .471
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Genee, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 3344 27-SEP-2001;
Millennium Pharmaceuticgis, Inc. (US)
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Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 9665 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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    .464
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CQ396273.1 GI:41304054
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SOURCE

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 15976 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 10979-A 4993 27-5EP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Sequence 4993 from Patent WO0170979.
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/db_xref="taxon:9606"
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CQ397922.1 GI:41305703
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 0142467-A 836 14-JUN-2001,
Millennium Predictive Medicine, Inc. (US)
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Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
compositions, kits, and method for identification,
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             assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 10775 27-SEP-2001, Millennium Pharmaceuticals, Inc. (US)
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Sequence 836 from Patent WO0142467.
AX185141.1 GI:15136522
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 017099-A 11286 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Query Match
1.4%; Score 24; DB 6; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels
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The invention relates to a novel isolated nucleic acid molecule comprising: a sequence encoding a sequence comprising 11-1518 amino acids ; a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polynucleotides of the invention can be used to treat disorders by gene therapy. This polynucleotide represents a breast specific related sequence of the invention
                                                                              New isolated nucleic acid molecule, useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer
Liu C;
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Pluta J,
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ò	1021	TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCC 1080	980
qq	1021	TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCC 108	980
ý	1081	ATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 114	140
QQ	1081		140
ò	1141		200
Db	1141	TTCCAGGGCACCGACACAGACTCGTCGGGGGCACCCTTGCTCCAGGTGTACTGCTAACCC 120	200
ò	1201		560
QQ	1201		560
ò	1261		320
Db	1261	GGACCAGGAACCCCTGTGGGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCC 132	320
ò	1321	TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 138	88
QQ	1321	TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 138	80
λ	1381	TCCTIGCATCCCCAGCTGGTCTGATCCCTGCCAGGCCCCCTTCCTT	140
Db	1381	TCCTTGCATCCCCAGCTGGTCTGATCCCTGCCAGGGCCCCTTCCTT	140
δλ	1441	TCAGGIGGCCIGATCAIGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGIGAACCCTG 150	905
Db	1441	TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 150	90
ò	1501	ACTCCATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTCC	999
Db	1501	ACTCCATCCCCTATTGCCACCCTAACCAATCATGCAACTTCTCCCTCC	999
È	1561	TCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATT	220
Ор	1561	TCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATT	220
δ	1621	CTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGGTGATGTTCTGTATCTTAACATGAC 168	280
ДD	1621	CTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTATCTTAACATGAC 168	980
ò	1681	881 CACAGITICIDAAGTACCTCGGCGACCACGC 1713	
QQ	1681	CACAGITIGIAAGIACCICGGCGGCGACCACGC 1713	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              designated NAAP-1 to NAAP-57. The human interact acturassociated procession antiarteriosclerotic, anti-HIV, antiallergic, cerebroprotective, antiarteriosclerotic, anti-HIV, antiallergic, cerebroprotective, antiartension, ophthalmological, thyromimetic, antiarthritic, hepatotropic, antibacterial, virucide, protozoacide, antiparasitic and fungicide activities, and can be used in gene therapy. The NAAP protein preventing diseases or conditions associated with the decreased expression or overexpression of NAAP, such as cell proliferative diseases. Ce.g. cancer, atherosclerosis, hepatitis), neurological disorders (Parkinson's disease, Alzheimer's disease, stroke, epilepsy), developmental disorders (renal tubular acidosis, anemia, glaucoma, topic dermatitis, arthritis) and minections (e.g. bacterial, viral, parasitic, protozoal, fungal). The present sequence encodes human NAAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human nucleic acid-associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,
                                                                                                                                       antiarteriosclerotic; anti-HIV; antialiergic; cerebroprotective; antiarteriosclerotic; anti-HIV; antialiergic; cerebroprotective; antiparkinsonian; anticonvulsant; nootropic; neuroprotective; antiarthritic; hepatotropic; antibacterial; virucide; protozoacide; antiparasitic; fungicide; gene therapy; cell proliferative disease; cancer; atherosclerosis; hepatitis; neurological disorder; Parkinson's disease; Alzheimer's disease; stroke; epilepsy; developmental disorder; renal tubular acidosis; anaemia; glaucoma; hypothyroidism; autoimmune disorder; inflammatory disorder; AIDS; allergy; atopic dermatitis; arthritis; infection; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes human nucleic acid-associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Burford N;
Elliott VS, Emerling BM, Forsythe IJ, Gorvad AE, Griffin JA;
Kable AE, Khare K, Lal PG, Lee EA, Lee SY, Li JX, Marquis JP;
Ramkumar J, Richardson TW, Sprague WW, Swarnakar A, Tang YT;
Chawla NK, Warren BA, Yue H;
                                                                                           Human nucleic acid-associated protein NAAP-41 cDNA SEQ ID NO:98
                                                                                                                          nucleic acid-associated protein; NAAP; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; SEQ ID NO 98; 405pp; English.
BP
ADD01260 standard; cDNA; 2392
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11-JAN-2002; 2002US-0347633P.
25-JAN-2002; 2002US-0359498P.
22-PEB-2002; 2002US-0359498P.
                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2002; 2002WO-US041115
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                                                            (first entry)
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Ramkumar J, Richardsor
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                              ADD01260
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DB 10; Length 2392;

Score 1645; Pred. No. 0;

96.0**%**; 99.9**%**;

Query Match Best Local Similarity

Sequence 2392 BP; 471 A; 743 C; 674 G; 504 T; 0 U; 0 Other;

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1 ATGCCCCGCCCTGGACACCCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG
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Ishii S; l, Tamechika I;

Otsuki T, Wakamatsu A, Sato H, Ish Hio Y, Otsuka K, Nagai K, Irie R, Otsuka M, Nagahari K, Masuho Y;

2003-450961/43.

HELIX RES INST. RES ASSOC BIOTECHNOLOGY.

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New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
       05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                as targets of gene therapy
                                                             Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                           P-PSDB; ADB64615
                                    (HELI-)
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                                            TTCCAGGCCACCGACACACACTCGTCGGGGCACCCTTGCTCCAGGTGTACTGCTAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; 88; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Clone KIDNE20157100 protein"
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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colypeptides. Also claimed is a polypeptide encoded by the polynucleotide, an antibody binding to the polypeptide or peptide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide of sis useful as a primer for synthesising the polynucleotide. On as a probe of or suseful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related conficients or medicines for regulation of their expression and activity, or as targets of genes may be included in their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, encoding them can be used as indicators for constant of reat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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Specification. Compilering any of the actions and control invention are useful for identifying, diagn control invention are useful for identifying, diagn control invention and treating lung cancer and non-car identifying and/or deeigning antagonists of convention, gene therapy, production of transcore encodes a lung specific nucleic acid axx cords and specific nucleic acid control invention. So sequence 1977 BP; 393 A; 631 C; 554 G; 399 Query Match control invention of transcore invention in the second control in the secon	1261 GGACCAGGAACCCTGTGGGAAGCTTAGAGGTGGCCTAAGAGTGAAGAGGG	
New isolated human nucleic acid molecule an identifying, diagnosing, monitoring, stagin cancer and non-cancerous diseases of the lu Claim 1; Page 266-267; 389pp; English.	INTIGENEGRACION CONTROLLI IN IN IN INTIGENEGRACION CONTROLLA IN INTIGENEGRACION CONTROLLA INTIGE	96 66 BB
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1441	361 GGGACTGCTGAAGCCAACTGGGCCAAATGGAGTGCCCCCCAGCCCTGATCGT 420	è q

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an nucleic acid (I) encoding any nces (S1), given in the 9-12421 base pair sequences (S2), and compositions of the present lagnosing, monitoring, stading, n-cancerous diseases of the lung. Lissue, monitoring and sof the polypeptide of the transgenic animals and production and research. This sequence
ATGCAAACTTCTCCCTCCCTGGGGTAAT 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
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Novel human polynucleotide SEQ ID NO 239.
BP
AEA19545 standard; cDNA; 791
                                       (first entry)
                                       11-AUG-2005
                   AEA19545
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RESULT 6 **AEA19545**

DNA purification; protein purification; osteoparthritis; antiarthritic; osteopathic; musculoskeletal disease; osteoporosis; endocrine disease; periodontal disease; antiinflammatory; mouth disease; burns; injury; peripheral neuropathy, Alaheimers disease; neuroprotective; nootropic; degeneration; parkinsons disease; antiparkinsonian; neurological disease; carebrovascular ischemia; cerebroprotective; vasotropic; cardiovascular disease; autoimmune disease; immunosuppressive; immune disorder; viral infection; virucide; infection; cancer; New polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g. osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral я, Y; Chen I mapping; Zhou P, Ma Goodrich R, forensic; vulnerary; CNS-gen.; gene therapy; diagnostic; Ψ, Q Ren I Wang I Claim 1; SEQ ID NO 239; 500pp; English. 'nά Zhang Zhao Q cytostatic; neoplasm; gene; ss Boyle B; 11-MAR-2004; 2004WO-US007412. Wang ZW, Asundi V, 14-MAR-2003; 2003US-00389559 infection, or cancer. Weng G, 2005-417730/42. (NUVE-) NUVELO INC. Wang J, Xue A, P-PSDB; AEA20112 WO2005049806-A2 Homo sapiens. 02-JUN-2005 Wehrman T, Tang TY, Ghosh M,

The invention describes a new isolated polynucleotide (I) encoding a polypeptide with biological activity comprising: a nucleotide sequence of polypeptide with biological activity comprising: a nucleotide sequence of (I) under stringent hybridization conditions; or a nucleotide sequence of (I) under stringent hybridization conditions; or a nucleotide sequence of (I) under stringent hybridization conditions; or a nucleotide sequence of (I). Also described are: a(I) (expression) vector comprising (I); a host cell genetically engineered to comprise (I) operatively, associated with a regulatory sequence that modulates expression of the polymetide in the host cell; an isolated polypeptide conditions with any one of SEQ is: a polypeptide encoded by (I); or a polypeptide encoded by a sequence of SEQ ID NOS: 568-1134 ([Mully defined), where the polypeptide of (SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3); a method carrier; an antibody directed against the polypeptide of (3); a method of ridentifying a compound that binds to the polypeptide of (3); a method for identifying a compound that binds to the polypeptide of (3); a method of polymucleotides, where the collection of (3); and a collection of polymucleotides, where the collection of (3); and a collection of polymucleotides, where the collection of (3); and a collection of polymucleotides, where the collection of (3); and a collection of polymucleotides, where the collection of sequences of SEQ ID NOS: 1-567. (I) is a polymucleotide comprising of a collection of polymucleotides, where the collection of activity, which comprises any of the amino acid sequences and methods are useful in diagnostics, forenic, and gene mapping, in identifying of mutations responsible for genetic disorders or composition and method are useful for treating a disease, burns, CN of partipheral disease, all parties, viral infection, or cancer. This sequence encodes a concodes a polymential of the polymential of the invention. novel polypeptide of the invention.

Sequence 791 BP; 149 A; 278 C; 222 G; 142 T; 0 U; 0 Other;

39.9%; Score 683; DB 14; Length 791;

Query Match

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                                                                                                                                                                                                                                                                                          The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-1421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, thousand non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence encodes a lung specific nucleic acid
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                                                                                                                                                 New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
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100.0%; Pred. No. 3.5e-174;
tive 0; Mismatches 0;
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(DIAD-) DIADEXUS INC
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The invention relates to a novel isolated nucleic acid molecule comprising: a sequence encoding a sequence comprising 11-1518 amino acids is a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polynucleotides of the invention can be used to treat disorders by gene therapy. This polynucleotide represents a breast specific related sequence of the
                                                                                                                                                                                                                                                                                         isolated nucleic acid molecule, useful for treating breast cancer, diagnosing or monitoring the presence of metastases of breast cancer
                           BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer; breast cancer; breast specific; human; ds.
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specific related polynucleotide SEQ ID No 104
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Matches 378; Conservative
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metastatic;
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                                                                                                                                                                                                                                                                                                                                                  The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCAGGAACCCCTGTGGGGAGAGGTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCTG 128
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 gene therapy; cytostatic; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                             a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                         Claim 1; Page 248; 367pp; English
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Best Local Similarity
Matches 378; Conservat
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ID ABT1
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AC ABT1
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DT 30-J
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1442

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1322

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128

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Gaps

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1045 ACAGTGCAGATCTCCCAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTAT 1104
                                                                                           261 ACAGTGCAGATCTCCCCAGGAGACGACTGCAGAGGCCATCGCCCGGAAGCTGAGGCCTTAT 320
                                  201 GCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is one of 1351 sequences in a library of human polymucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polymucleotides on the probes can be used for chromosome mapping of the polymucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polymucleotides and their gene products are used as genetic or blochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and antibodies against them can be used in pharmaccutical compositions to treat the cancers and proliferative disorders such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klinger J;
Pot D, Lamson (
Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human, cytostatic, gene therapy; colon cancer, prostate cancer; breast cancer; lung cancer; cancer detection; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams LT, Escobedo J, Innis MA, Garcia PD, Kilinger J;
Kassama A, Reinhard C, Randazzo F, Kennedy GC, "Pot D, Lam
Drmanac R, Crkenjakov, Drmanac S, Dickson M, Labat I;
Leshkowitiz D, Kita D, Garcia V, Jones LW, Strache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 427 BP; 69 A; 161 C; 123 G; 73 T; 0 U; 1 Other;
                                                                                                                                            GGAGCTCCAGGGTACCCAGCAAGCCATGACTCAT 1138
                                                                                                                                                               GGAGCTCCAGGGTACCCAGCAAGCCATGACTCAT 354
                                                                                                                                                                                                                                                                                                                                                                                     Novel human polynucleotide, SEQ ID NO: 2132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.7%; Score 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 854; 1046pp; English.
                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                          AAF66376 standard; cDNA; 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000WO-US018374.
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99US-0142311P.
                                                                                                                                                                                                                                                                                                                                              09-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1999;
02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2001.
                                                                                                                                                                                                                                                                                                              AAF66376;
                                                                                                                                            1105
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985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of 3351 sequences in a library of human polymucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polymucleotides. The probes can be used for chromosome mapping of the polymucleotides. The probes can be generated. The polymucleotides and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polymucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carringenesis pathway and/or monitor the efficacy of therapies and preventions. The polymucleotides along the antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCT 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lamson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences.
                                                                                                                                                          cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; ss.
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Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lam
Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
Leshkowitiz D, Kita D, Garcia V, Jones LW, Strache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 334; DB 5; Le
Pred. No. 1.1e-149;
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19.5%; Score 334; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 334; Conservative 0; Mismatches
                                                                                                                         Novel human polynucleotide, SEQ ID NO: 177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 570; 1046pp; English.
                 AAF64421 standard; cDNA; 393 BP.
                                                                                                                                                                                                                                                                                                                             30-JUN-2000; 2000WO-US018374.
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                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                     WO200102568-A2.
                                                                                                                                                                                                                 Homo sapiens.
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02-JUL-1999;
                                                                                                                                                                                                                                                                                         11-JAN-2001.
                                                                                     09-APR-2001
                                                 AAF64421;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                         200 CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACATGGGCCAGAGAGCATTACCTTC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTCTGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCTGCTCTGCTCTGGGGACCC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGTGTGGGGGTGCCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG 300
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                                                                                1 ATGCCCCGCCCTGGACACCCCCCCCCCGCCATCTGGGCCCTCCACGCTTGGGACCGTGGGAG
                                                                                                                                                                                          CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC
                                                                                                                                                                                                                                                                                                      CGCACCCGTAGACCAGGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGATTACCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
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Randazzo F, Kemnedy GC, Pot D, Kassam
Crkvenjakov R, Dickson M, Drmanac S, I
Garcia V, Jones WL, Stache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene expression product cDNA sequence SEQ ID NO:861
                         Indels
100.0%; Pred. No. 2e-143; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCTGTGGAGCCTGTGTGCGG 400
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98US-0080114P.
98US-0080515P.
98US-0105234P.
98US-0105877P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                         321, Conservative
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Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
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  Similarity
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Best Local
Matches 32
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AAZ13392

ID AAZ13392

ID AAZ13392

ID AAZ13392

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The present invention describes a library of human polynucleotides

comprising the sequences given in AAZ12532 to AAZ1779. Also described is

cancerous state of a mammalian cell, comprising detecting at least one

differentially expressed gene product in a test sample from a cell

cancerous state of a mammalian cell, comprising detecting at least one

differentially expressed gene product in a test sample from a cell

concerous state of a mammalian cell, comprising detecting at least one

differentially expressed gene product in a test sample from a cell

conserved of being cancerous, where the gene product is encoded by one of

the 5248 polymucleotide sequences given in AAZ12532 to AAZ17779. The

polymucleotides can be used as a source of primers and probes, which can

conserved for a variety of purpose, e.g. detection of expression levels,

mapping, tissue typing or profiling, forensics, genetic analysis and

detection of polymorphisms. Polypeptides encoded by the polymucleotides

concerved a seaf for raising antibodies for experimental, diagnostic and

therapeutic purposes. The polymucleotides may also be used to construct

arrays for diagnostics (which may be used to determine function of an

concerls (e.g. to identify abnormal or diseased tissue in a human, to

diagnosis, prognosis and management of colorectal cancer, breast cancer,

and lung cancer. The polymucleotides can also be used to screen for

peptide analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 300; DB 2; Le
Pred. No. 2.5e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.5%; Scor.
100.0%; Pred. No. c...
'... 0; Mismatches
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Matches 300;
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TCTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCGCTGTGGAG 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 248; 367pp; English.
                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                             ABT07645 standard; cDNA; 654
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Matches 222; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIAD-) DIADEXUS INC
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                                                                                                                                                                                                                                                                                                                                         14-NOV-2002
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920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel isolated human polymucleotides obtained by screening for differential expression in colon cancer, breast cancer and lung acancer call lines. The polymucleotides of the invention are represented in AAX98275-X99118 and encode polypeptides of protein families selected from 4 transmembrane segments integral membrane callular activities (AAA), eukaryotic aspartyl proteases, GATA family of transmeription factors, G-protein apha subunit, phorbolesters or diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, cranscription factors, G-protein apha subunit, mortaining proteins. The croaded polypeptides also have a functional domain selected from Ank repeat, basic region plus leucine zipper transcription factors, crepett, basic region plus leucine zipper transcription factors, crepett, basic region plus leucine zipper transcription factors, commodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (CCHC class), and zinc-binding metalloprotease (C domain, The polymucleotides encode polypeptides with similarity to known protein families and are predicted to have similar properties. The novel copynucleotides can be used to develop products for use as therapeutic agents and in forensics, genetic analysis, mapping and diagnostic complications. In particular, the product can be used for treating e.g. cervical cancers, melanomas, colorectal adenocarcinomas, wilm's tumour, sarcomas, cretinolary encodermia, promyelocytic leukemia, monocytic leukemia, and lymphomas euch as histiocytic lymphoma, and management of cancers. They can be used for treating e.g. myeloid leukemia, and lymphomas euch as histiocytic lymphoma, and management of cancers in ung carcinomas, leukemias, and encodermal dysplasia, congenital alveolar dysplasia, and encodermal dysplasia, congenital alveolar dysplasia of the cervix, fibrous dysplasia, defended encodermal dysplasia, hyperplasias, e.g. endometrial, adrenal, breast, c.c. h.c. e.g. endometrial, adrenal, hyperplasias or pseudoepplemented or pay
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                                                                                                                                                                                                                                                                                            Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                        Escobedo J, Innis MA, García PD, Sudduth-Klinge
Jises K, Randazzo F, Kennedy GC, Pot D, Kassam
nanac R, Crkvenjakov R, Dickson M, Drmanac S, L
Kita D, García V, Jones LW, Stache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 300 BP; 68 A; 90 C; 86 G; 56 T; 0 U; 0 Other;
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Pred. No. 7.9e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 326; 591pp; English.
                                                                                                         98US-0080664P.
98US-0105234P.
98US-0105877P.
                                            98WO-US027610.
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Best Local Similarity 99.7%;
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                              Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                        Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
                                                                                                                                                                                                                           CORP.
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                                                                                                                                                                                                                        (CHIR ) CHIRON COR (HYSE-) HYSEQ INC.
                                          22-DEC-1998;
                                                                                                            03-APR-1998;
21-OCT-1998;
                                                                                                                                                      27-OCT-1998;
21-DEC-1998;
                                                                                       23-DEC-1997
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                                                                                     241 CCGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGGCCTCAGGTCTCAGCCAGGATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New breast specific nucleic acids and proteins, useful for identifying,
                                                     CCGCTGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 creeccaccareeeccaeaeaecarraccrrcarcrcrecrecrecreaccecceccrris
181 GAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGGCTGCTGCCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 ATGATAAACCACCTCAGCCCCCACCAAGCCGCCGCACCCGTAGACCAGACCCCAAGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, breast specific gene, breast specific protein, breast cancer, gene therapy, cytostatic, gene, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing, monitoring, staging, imaging, and treating breast cancenon-cancerous disease states in breast tissue, and in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Lo. Score 222; DB 6; Lengu...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCGCTGTGGAG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hu P, Recipon H, Karra K,
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100.0%; Pred. No. 7.4e-
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Homo sapiens
                                                                               WO9938972-A2
                                                                                                                            28-JAN-1999;
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                                                                                                                                                                                                03-APR-1998;
21-OCT-1998;
                                                                                                      05-AUG-1999.
                                                                                                                                                   28-JAN-1998
                                                                                                                                                               24-FEB-1998
                                                                                                                                                                         31-MAR-1998
                                                                                                                                                                                      03-APR-1998
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                                                                                                                                                                                                                                                         (HXSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH69926/c
ID AAH6992
XX
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1575 AAGCTTATCTTAAATGTATTGTATTGGGGGGTGGGCCAGGGCCCACTCTATGTTATGTTAA 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1635 GGAGTTGGTTCTTGGCTGATGTTCTGTATCTTAACATGACCACAGTTTGTAAGT 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                           of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antegonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AAGCTTATCTTAAATGTATTGTATTGGGGGGGGGGCAGGCCCACTCTATGTTAAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGTTGGTTCTGGCTTGTTGTTCTTGTATCTTAACATGACCACAGTTGTAAGT 1
                                                                                                                                                                                                                                                                                                                                                             New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes an isolated human nucleic acid (I) encoding any
                                                                                                                         Human; gene therapy, vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene expression product cDNA sequence SEQ ID NO:4887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 120 BP; 45 A; 33 C; 17 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.0%; Score 120; DB 6; I
larity 100.0%; Pred. No. 7.6e-47;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                  Liu
                                                                                                                                                                                                                                                                                                                  Sun X,
                                                                                                     Lung specific nucleic acid (LSNA) #116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encodes a lung specific nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 266; 389pp; English.
                                  ABX92074 standard; cDNA; 120 BP
                                                                                                                                                                                                                                                                                                                 Chen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ17414 standard; cDNA; 728 BP.
                                                                                                                                                                                                                                             21-NOV-2001; 2001WO-US043612.
                                                                                                                                                                                                                                                                    22-NOV-2000; 2000US-0252500P.
                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                  Macina RA, Recipon H,
                                                                                                                                                                                                                                                                                           (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                       WPI; 2002-713376/77.
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Matches 120; Conserva
                                                                                                                                                                                                 WO200268633-A2
                                                                                                                                                                          Homo sapiens
                                                                               08-MAY-2003
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                                                                                                                                                                                                                        06-SEP-2002
                                                       ABX92074;
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          RESULT 15
                       ABX92074/
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The present invention describes a library of human polymucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the productides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polymocleotides can be used for raising antibodies for experimental, diagnostic and detection of polymorphisms. Polypeptides encoded by the polymocleotides can be used for raising antibodies for experimental, diagnostic and construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two calls (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic purposes. The polymocleotides of the invention are especially used in the diagnosis, prognosis and management of colorects, cancer, and management of colorects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human genes and their expression products which are differentially expressed in different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Garcia V, Jones WL, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sudduth-Klinger J;
                                    detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists
Human; gene; gene expression product; diagnosis; therapy; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Garcia PD,
Kennedy GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.2%; Score 38; DB 2; Le
.00.0%; Pred. No. 1.9e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 2323-2324; 2479pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH69926 standard; cDNA; 323 BP.
                                                                                                                                                                                                                                                                                                                                                                                                            98US-0072910P.
98US-0075954P.
98US-0080114P.
98US-0080155P.
98US-0080666P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Reinhard C, Giese K, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-494092/41.
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Best Local Similarity
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New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is affilicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, ovarian cancer, identification; detection; characterisation; tumour; kinase; marker; cytostatic; antisense gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 329 BP; 106 A; 45 C; 59 G; 119 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ovarian cancer cell expressed sequence 3785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 1.6%; Score 28; DB 4;
Local Similarity 100.0%; Pred. No. 0.012;
Nes 28; Conservative 0; Mismatches (
                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1686 TTTGTAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                               Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 TITGIAAGTACCTCGGCCGCGACCACGC
                                                                                                                                                                                                                                                                                                    Claim 1; Page 226; 1051pp; English.
                                                                                                                                                                             Berger A,
              08-DEC-1999; 99US-0169681P.
21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAY-2000; 2000US-0203791P.
09-UTM-2000; 2000US-0210600P.
21-UUL-2000; 2000US-0220114P.
              990S-0169681P.
990S-0171350P.
2000US-0189315P.
2000US-0203791P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee J, Thompsho P, Lillie J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2000; 2000US-0190347P.
21-MAR-2000; 2000US-0191321P.
31-MAY-2000; 2000US-0208382P.
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AAF98612 standard; DNA; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2001 (first entry)
                                                                                                                                                                               Deeds J,
                                                                                                                                                                                                              WPI; 2001-375006/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-1999;
                                                                                                                                                                             Schlegel R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF98612;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                        Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
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Pred. No. 0.012;
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                                                                    Human cervical cancer marker nucleic acid 1200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cervical cancer marker nucleic acid 712.
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                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITGIAAGIACCICGGCCGCGACCACGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 294; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH69438 standard; cDNA; 329 BP
                                                                                                                                                                                                                                                                                 08-DEC-1999; 99US-0169681P.
21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAY-2000; 2000US-0203791P.
                                                                                                                                                                                                                                                  08-DEC-2000; 2000WO-US03312.
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                                                                                                                                                                                                                                                                                                                                                          2000US-0210600P
                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-375006/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                         Homo sapiens.
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                                 19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                            09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlegel R,
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AAH69926;
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Gaps

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Length 329; Indels

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WO200142467-A2.
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14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                       19-SEP-2001
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                                                                                                                                                                                                                                            AAH70907;
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                                                                                                                                                                                        RESULT 21
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                                                                          marker (1) (see AAF9854 to AAF98730), in a control non-ovarian cancer sample, mormal level of expression of (1) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (I) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated hybridoma, which produces an antibody useful for ovarian cancer assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to AAF98593 represent human kinase marker primers and probes which are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for
                                                    s present invention describes a method for assessing whether a patient afflicted with ovarian cancer by comparing: (1) the expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
 comprises detecting changes in the expression of a variety of markers.
                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                   1.5%; Score 26; DB 5; Length 91;
100.0%; Pred. No. 0.11;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                            Sequence 91 BP; 23 A; 17 C; 20 G; 31 T; 0 U; 0 Other;
                                                                                                                                                                                                                 in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cervical cancer marker nucleic acid 1358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berger A, Zhao X;
                                                                                                                                                                                                                                                                                                                            1688 TGTAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 314; 1051pp; English.
                          Claim 1; Page 988; 1198pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                        ₽.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1999; 99US-0169681P.
21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAY-2000; 2000US-0210591P.
09-UUN-2000; 2000US-0210690P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0220114P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schlegel R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition; to monitor the and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
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                                                                                                                   Length 203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cervical cancer marker nucleic acid 2181.
                                                                                                                   DB 4;
0.11;
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.00.0%; Pred. No. 0.11;
.ve 0; Mismatches
                                                                    Sequence 203 BP; 52 A; 41 C; 59 G; 51 T; 0 U;
                                                                                                                                    100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao X;
                                                                                                                                                                                                                 1688 TGTAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                   Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTAAGTACCTCGGCCGCGACCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 461; 1051pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlegel R, Deeds J, Berger A,
                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0169681P.
99US-0171350P.
200US-0189315P.
200US-0203791P.
2000US-0210600P.
                                                                                                                                                                                                                                                                                                                                                                                   AAH70907 standard; cDNA; 412
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                                                                                                                      1.5%;
                                                                                             Query Match
Best Local Similarity luv..
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 100.
Matches 26; Conservative
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WO200257414-A2
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 Homo sapiens.
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                                       25-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                 invention
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ABV37465/c
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                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and polypeptides are also useful for isolating compounds with cytostatic polypeptides are also useful for isolating compounds with cytostatic
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                                                                                                                                                                                                                                                                                                                                      New peptide useful as a marker for the diagnosis of breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 26; DB 4; Length 576;
llarity 100.0%; Pred. No. 0.11;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 576 BP; 134 A; 111 C; 125 G; 205 T; 0 U; 1 Other;
                                                                    Human breast cancer expressed polynucleotide 9868.
                                                                                      Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human leukocyte derived cDNA SEQ ID NO 8473.
                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 TGTAAGTACCTCGGCCGCGACCACGC 575
                                                                                                                                                                                                                                                                                               Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 1758; 3695pp; English.
       AAL17411 standard; cDNA; 576 BP
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                                                                                                                                                                                                    14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193460P.
15-MAY-2000; 2000US-020530P.
09-UNM-2000; 2000US-0211315P.
25-UUL-2000; 2000US-020534P.
                                                                                                                                                                       10-JAN-2001; 2001WO-US000798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ08482 standard; cDNA; 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                               (first entry)
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hes 26; Conserv
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                                                                                                                               WO200151628-A2.
                                                                                                            Homo sapiens
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                                               07-DEC-2001
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                                                                                                                                                                                                                                                                                              Lillie J,
                           AAL17411;
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Matches
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The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ003152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, 88.
                                                                                                                                                                                                                                                                                                                                                                                              New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                   Phillips J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is that of a human leukocyte expressed cDNA of the
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                                                                                                                                                                                                                                      Prentice J,
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                                                                                                                                                                                                                                   Altman P, P.
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100.0%; Pred. No. 0.34;
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                                                                                                                                                                                                                                   K, Matcuk G, A
Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 26; Page 1920; Opp; English.
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22-OCT-2001; 2001WO-US047856.
                                                                 20-OCT-2000; 2000US-0241994P.
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16-MAR-2000; 2000US-0189862P.
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Ly N, Woodward R, Qu
                                                                                                                                                                 (BIOC-) BIOCARDIA INC
                                                                                                                                                                                                                                                                                                                                   WPI; 2002-636525/68.
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Homo sapiens
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                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                            invention.
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                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; determining whether prostate cancer has metastasized in a patient; (l) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                       Score 25; DB 5; Length 255;
Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                    Sequence 255 BP; 56 A; 55 C; 80 G; 64 T; 0 U; 0 Other;
                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ovarian cancer DNA marker #17410
                                                                                                                                                                                                                                                                                                                                                                                                     97 Graagraccreeecceceaccacec 73
                                                                                                                                                          Claim 1; Page 7689; 11750pp; English.
                                                                        Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                       Match 1.5%; Scc
Local Similarity 100.0%; Pi
es 25; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
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15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
         2000US-0211314P
                                                                                            WPI; 2001-662795/76.
25-MAY-2000;
09-JUN-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides concerous) ovarian calls. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the conception ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonucleotide complementary to a marker of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of a marker in a patient sample and a normal level of expression of the expression levels indicates ovarian cancer. The level of expression of a marker or a secreted protein or to a transcribed compared to responds to a secreted protein or to a transcribed compared to a secreted protein or to a transcribed compared to a secreted protein or to a transcribed compared to a secreted protein or protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed compared by detecting the marker, under stringent conditions. The polynucleotide ownics with the marker or anneals with a portion of the polynucleotide which anneals with the marker or anneals with a patient compared or expression of the marker is also used for monitoring the presence of a transcribed comparising the marker or anneals with a patient or sample at a first point in time, repeating the marker or a subsequent contained and comparing the level of expression. He marker is a subsequent of expression of the marker is a pared to be a second or a pared to be a second or a pared or a p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using an ovarian Lissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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Pred. No. 0.34;
                                                                                                                                                                                               SEQ ID NO 17410; 106pp; English.
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16-MAR-2000; 2000US-0189862P.
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Best Local Similarity 100.
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                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer and many determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
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                                                                                                                              Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                               assessing the aggressiveness or indolence of prostate cancer in a pat i (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 304 BP; 80 A; 63 C; 78 G; 76 T; 0 U; 7 Other;
                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Preα. ...
've 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ovarian cancer DNA marker #11387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 GTAAGTACCTCGGCCGCGACCACGC 15
                                                                                                                                                                                Claim 1; Page 1214; 11750pp; English.
                                                                                  Monahan JE;
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           2000US-0211314P.
2000US-0219007P.
                                   13-DEC-2000; 2000US-0255281P.
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2000US-0207124P.
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2000US-0220661P.
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                                                                                                       WPI; 2001-662795/76
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Best Local Similarity
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           09-JUN-2000;
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25-MAY-2000;
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                                                                                 Schlegel R,
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                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncancerus) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concernus) ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of the invention. The markers and a normal level of expression of the marker in a patient sample and a normal level of expression of the expression levels indicates ovarian cancer. The level of expression of a marker ordersponds to a secreted protein or to a transcribed comparing to the marker. The presence of protein or protein cransponding to the marker. The presence of protein or protein cransponding to the marker. The presence of expression of the marker is assessed by detecting the presence in the sample, a protein or protein cransponding to the marker. The presence of a transcribed comparising to the marker, under stringent conditions. The polynucleotide which anneals with the presence of a transcribed colynucleotide which anneals with the presence of a transcribed colynucleotide which anneals with the presence of a transcribed colynucleotide which anneals with the presence of a transcribed comparising the marker, under stringent conditions. The marker is also used for monitoring the presence of a transcribed column or protein the intent propersion of the marker in a protein or protein of expression of the marker in a patient which involves detecting expression of the marker in a patient which involves detecting expression of the marker in a patient which involves detecting expression. The marker in a patient of expression of the marker in a practical marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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Pred. No. 0.34;
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100.0%; Pred. No. c..
                                                                                                                                               Disclosure; SEQ ID NO 11387; 106pp; English.
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nes 25; Conservative
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Human; breast cancer; cell marker; cytostatic; ss.
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Best Local Similarity
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15-MAY-2000;
                                                  Ношо варіепв
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to nucleic acid markers which are overaxpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancercus) ovarian cells. The invention also relates to polypeptides cancercus) ovarian cancer intibodies that selectively bind to the canceded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclecide complementary to a marker of the invention. The markers are useful for assessing it a patient is afflicted with ovarian cancer sample. A difference between the amarker in a patient sample and a normal level of expression of a marker ortresponds to a secreted protein or to a transcribed of expression of the marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker or anneals with a portion of the polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker or anneals with a portion of the polynucleotide which anneals with the marker or anneals with a specient or protein time, repeating the marker in a patient sample at a first point in time, repeating the method is carried out time and comparing the level of expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression of the marker of the printed or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer presence of the printed specification, but was obtain
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                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
                                                                                                                                                                                                                                                                                                                            cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 5; Length 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the printed specification, but was obtained in electro
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 310 BP; 91 A; 72 C; 73 G; 74 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.34;
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                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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               15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
25-JUL-2000; 2000US-0220661P.
                                                                                              2000US-0257672P
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                                                                                              21-DEC-2000;
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                                                                                                                                                                                                Lee J,
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Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide useful as a marker for the diagnosis of breast cancer.
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Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 v 100.0%; Pred No.
                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAY-2000; 2000US-0203791P.
                                                                                   2000US-0189167P.
2000US-0192099P.
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2000US-0205230P.
2000US-0211315P.
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10-JAN-2001; 2001WO-US000798
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity (c) (a); or (f) degenerate variants of (a). Polypeptides (ABP68595-C) ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and probes or primers for nucleic acid hybridisation, in the design and compositions and proteins in the tumour colls, in vaccines and for gene therapy. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                 SEQ ID NO 4393; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                       Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                         Sequence 453 BP; 100 A; 93 C; 131 G; 129 T; 0 U; 0 Other;
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2000US-0207124P.
2000US-0211940P.
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                                                                                                                                                                                                                                                                                                                                                                                                                      25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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25-MAY-2000;
15-JUN-2000;
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                                 Claim 1;
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    cancer.
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                                                                                                                                           New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                       The invention relates to novel genes (AAH68727-AAH73383) associated with occivical cancer with cytostatic activity. The nuclaic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
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cytostatic; tumour; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human pancreatic cancer expressed cDNA SEQ ID NO 4393.
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.5%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 0.3 Matches 25; Conservative 0; Mismatches
                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                              Zhao X;
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                                                                               Berger A,
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12-JUL-2001; 2001US-0305484P.
20-AUG-2001; 2001US-0313999P.
09-JUN-2000; 2000US-0210600P
21-JUL-2000; 2000US-0220114P
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2001US-0267568P.
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                                                                                                                                                                                                                                                                                                                                          useful for gene therapy
                                                                              Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benson DR, Kalos MD,
                                                                                                             WPI; 2001-375006/39
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09-FEB-2001;
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                                                                              Schlegel R,
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cancerous) ovarian cells as compared to their expression in normal (i.e. noncarcerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cells. The invention also relates to polypeptides corceded by the markers, antibodies that selectively bind to the cold developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer which involves comparing the level of expression of the invention. The marker are useful for assessing if a patient is afflicted with ovarian cancer which involves comparing the level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels is didicates ovarian cancer and if expression of the marker corresponds to a secreted protein or to a transcribed of samessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the protein or protein creaments with a marker or anneals with a portion of the marker is assessed by detecting the marker or anneals with a portion of the polynucleotide comprising the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of expression of the marker is also used for monitoring the progression of the marker in a satiant which in an antiport of the marker or anneals with a partion of the marker is also used for monitoring the progression of the marker in a partion of the marker in a pration of the marker in a partion of the marker in a pration of the marker in a partion of the marker in a protein or protein in a partion of the marker in a partion of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ention. Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly
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100.0%; Pred. No. 0.34;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 463 BP; 123 A; 110 C; 117 G; 113 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 100.
Matches 25; Conservative
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Sun Y;
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The invention describes a breast specific nucleic acid. The nucleic acids, polypeptides, antibodies, agonists and antagonists, and compositions comprising them are useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and noncancerous disease states in breast tissue, in gene therapy, vaccine engineered breast tissue for treatment and research. The nucleic acids may be used as molecular markers for detecting breast cancer for accurate staging of the disease and monitoring the progress of cancer for accurate staging of the disease and monitoring the progress of cancer treatments, and as hybridisation probes or primers. This sequence encodes a breast specific protein of the invention
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                                                         cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
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                                                         diagnosing, monitoring, staging, imaging, and treating breast canconon-cancerous disease states in breast tissue, or for gene therapy
                                    New breast specific nucleic acids and proteins, for identifying,
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 810 BP; 216 A; 183 C; 145 G; 266 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 25; DB 6;
100.0%; Pred. No. 0.34;
tive 0; Mismatches
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                                                                                                                  Claim 1; Page 156; 227pp; English.
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WPI; 2002-657590/70.
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RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel method for monitoring differential expression of genes in a filamentous fungal cell. Specifically, it refers to identifying differential gene expression occurring between two related filamentous fungal cells and comprises adding detection reporter labeled nucleic acids of filamentous fungal cells to a substrate array of richoderma reses (Trichoderma reses) expressed sequenced tags (BSTS), or suppression subtractive hybridization (SSH) clones and detecting a signal in the array. The present invention further describes a computer readable medium having for monitoring differential expression of several genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells. It also provides a search unit for comparing a target sequence to a T. resesi BST sequence of the data storage unit to identify homologous sequences, and a retrieval unit for obtaining the homologous sequence (s). Accordingly, it provides a method useful for identifying microbial genes induced when the discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Note that this method utilizes an array where one spot equals or
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in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T_reesei suppressive subtractive hybridization (SSH) cDNA clone Seq 1051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monitoring differential expression of genes of two filamentous fungal cells, for e.g. discovering new genes, comprises adding labeled nucleic acids to an array of Trichoderma reesei expressed sequenced tags and
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                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression; suppressive subtractive hybridization; microarray;
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                                                                                                       Sequence 1252 BP; 269 A; 229 C; 238 G; 336 T; 0 U; 180 Other;
                                                                                                                                                 1.5%; Score 25; DB 11; Length 1252; 100.0%; Pred. No. 0.34; ative 0; Mismatches 0; Indels
                                                                    Bite at segdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                       1689 GTAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                           224 GTAAGTACCTCGGCCGCGACCACGC 200
                                                                                                                                                                                                                                                                                                                                                                                     ADY99697 standard; cDNA; 150 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypocrea jecorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microorganism; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ADY99697;
                                                                                                                                                                                                                                                                                                                                                                     ADY99697/c
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The invention relates to an isolated polymucleotide which encodes an immune related protein or a protein exhibiting biological properties of an immune-related protein with a sequence selected from 26 sequences. The expression vector and reagant are useful for the preparation of a capture such as allergic, autoimmune, inflammatory or infectious diseases, e.g. asthma, allergic, autoimmune, inflammatory or infectious diseases, e.g. asthma, allergic rhinitis, atopic dermatitis, hives, conjunctivitis, systemic lupus erythematosus, myasthenia gravis, psoriasis, sepsis, gout, or colitis. The polypeptides may also be used to identify compounds which may act as activators or inhibitors at the ciryme's active site, to raise specific antibodies which can block the cryme and effectively reduce its activity, as a bait protein in a two-hybrid or three-hybrid assay to identify other proteins which bind to or interact with the human immune-related protein and modulate its activity, and for immunisation of mammals. The polymucleotides of the invention can
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microarrays can be organized based on function of the gene products. This polynuclectide sequence is a T. reesei SSH cDNA clone that forms part of the substrate array of the invention. NOTE: The SeqIDB 1-1188 referring to T. reesei SSTB or SSH clones or their combinations are available in electronic form from the USPTO web site (http://seqdata.uspto.gov/sequence.html; Document ID:20050069934).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antiallergic, antiinflammatory; antiasthmatic; dermatological; ophthalmological; immunosuppressive; immune related; allergic ruinitis; autoimmune; inflammatory; infectious disease; asthma; allergic rhinitis; atopic dermatitis; hives; conjunctivitis; systemic lupus erythematosus; myasthenia gravis; psoriasis; espsis; gout; colitis; immunisation;
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                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 150;
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1.44; occidents 1, 198; Pred. No. 1;
Best Local Similarity 100.04; Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; mouse; murine; ds
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covarian cancer cells as compared to their expression in normal (i.e. non-
covarian cancer cells as compared to their expression in normal (i.e. non-
cancerous) ovarian cells. The invention also relates to polypeptides
conceded by the markers, antibodies that selectively bind to the
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a patient sample and a normal level of expression of
corresponds to a secreted process. The level of expression of a
corresponds to a secreted process. The level of expression of a
corresponds to a secreted process or transcribed
corresponding the presence in the sample, a protein or protein
corresponding to the marker. The presence of protein or protein
corresponding to the marker. The presence of protein or protein
corresponding to the marker. The presence of protein or protein
corresponding to the marker. The presence of protein or protein
corresponding to the marker. The presence of protein or protein
corresponding to the marker. The presence of protein or protein
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be used in gene therapy for treating disorders. This sequence represents an immune-related mouse protein of the invention. This polynucleotide represents an immune-related mouse DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to nucleic acid markers which are overexpressed in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                               8; Length 232;
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                                                                                      Sequence 232 BP; 52 A; 43 C; 49 G; 86 T; 0 U; 2 Other;
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100.0%; Pred. No. 1;
...ve 0; Mismatches
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2000US-0211940P.
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2000US-0220661P.
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                                                                                                                                                                                                                                                                                                                                                               ADL43332 standard; DNA; 253
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                         Query Match 1.4°
Best Local Similarity 100.
Matches 24; Conservative
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                the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method at a subsequent using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted
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protein fragment. Alternatively, the level of expression of
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                                                                                                                                                                                                                                                                     Sequence 253 BP; 44 A; 65 C; 65 G; 79 T; 0 U; 0 Other;
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100.0%; Pred. No. 1;
Live 0; Mismatches
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25-MAY-2000; 2000US-027124P.
15-UTN-2000; 2000US-0211940P.
07-UUL-2000; 2000US-0216820P.
25-UUL-2000; 2000US-022661P.
21-DEC-2000; 2000US-0257672P.
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                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                 invention.
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ADL37742/c
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with ovarian cancer, which involves comparing the level of expression of marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment or protein an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide comprising the marker or anneals with a portion of the polynucleotide comprising the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the marker in a subsequent than a comparing the level of expression.
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                                                                                                                                                                                                                                                                                                                         using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   invention
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The invention relates to nucleic acid markers which are overexpressed in

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cancerous) ovarian cells as compared to their expression in normal (i.e. non-
cancerous) ovarian cells. The invention also relates to polypeptides
canced by the markers, antibodies that selectively bind to the
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invention and a method of treating a
corresponding to a marker of the invelves complementary to a marker of the
invention. The markers are useful for assessing if a patient is afflicted
with ovarian cancer, which involves comparing the level of expression of
commarker in a control non-ovarian cancer sample. A difference between the
corresponds to a secreted protein or to a transcribed
complement is detecting the presence in the sample, a protein or protein
corresponding to the marker. The presence of protein or protein
corresponding to the marker. The presence of protein or protein
corresponding to the marker. The presence of protein or protein
corresponding to the marker. The presence of stranscribed
corresponding to the marker. The presence of a transcribed
correction fragment is detected using an antibody that specifically binds with the
correction or protein fragment. Alternatively, the level of expression of
colynuclectide which anneals with the marker or anneals with a portion of
construction or protein fragment. The marker or anneals with a portion of
construction or protein fragment is detecting the marker or anneals with a portion of
colynuclectide which anneals with the marker or anneals with a portion of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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100.0%; Pred. No. 1;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 274 BP; 79 A; 63 C; 63 G; 69 T; 0 U; 0 Other;
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2000US-0220661P.
2000US-0257672P.
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25-JUL-2000;
21-DEC-2000;
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70.

Lillie J;

Lee J,

07-JUL-2000; 2000US-0216820P. 25-JUL-2000; 2000US-0220661P. 21-DEC-2000; 2000US-0257672P.

2000US-0211940P

21-MAR-2001; 2001WO-US009126

21-MAR-2000; 15-JUN-2000; 25-MAY-2000;

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concernation and the properties are those involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of with ovarian cancer, which involves comparing the level of expression of marker in a patient sample and a normal level of expression of the expression levels indicates ovarian cancer. The level of expression of a marker or a secreted protein or to a transcribed complement or protein the presence in the sample, a protein or protein cancer fragment corresponding to the marker. The presence of protein or protein cancer fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is a sasessed by detecting the presence of a transcribed comprised by detecting the presence of a transcribed compression or protein or protein fragment. Alternatively, the level of expression of the marker is a sasessed by detecting the presence of a transcribed polynucleotide which anneals with the marker, under stringent conditions. The marker, under stringent conditions. In a marker is a sasessed by detecting the presence of a transcribed compression of the marker is a sasessed by detecting the presence of a transcribed marker is a sasessed by detecting the presence of a transcribed marker is a sasessed by detecting the presence of a transcribed marker is a sasessed by detecting the presence of a transcribed contraction or protein detected using the propersory of the marker is a sasessed by detecting the presence of a transcr
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                                                                                                       Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian of this sequence represents a human ovarian cancer DNA marker of the
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                                                                                                                                                                                                              Disclosure; SEQ ID NO 16395; 106pp; English
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10.0%; Pred. No. 1;
Best Local Similarity 100.0%; Pred. No. 1;
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Lillie J;
  Lee J,
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. nonceration cancerus) ovarian cells. The invention also relates to polypeptides cancerous) ovarian calls. The invention also relates to polypeptides cancerous) ovarian cancer intolving inhibiting expression of a gene corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to calls of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of the cappession levels indicates ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a carresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence of the protein or protein fragment is detected using an antibody that specifically binds with the frome or protein fragment. Alternatively, the level of expression of the marker is as oused for manitoring the presence of a transcribed polynucleotide comprising the presence of a transcribed comprising the anneals with a portion of the marker is as oused for manitoring the presence of covarian cancer in a patient which involves detecting the presence of covarian cancer in a patient which involves detecting the presence of covarian cancer in a patient which involves detecting the presence of covarian cancer in a patient comprising the level of expression of the marker is also used for manitoring the marker is used to ormanial with the marker is used for manitoring the marker is used to ormanial with 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 310 BP; 72 A; 54 C; 66 G; 118 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3678; 106pp; English.
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100.0%; Pred. No. 1;
tive 0; Mismatches
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Best Local 8
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1D ADI772

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ADL36491 standard; DNA; 312 BP

ADL36491/c RESULT 43

20-MAY-2004

ADL36491;

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian calcs. The invention also relates to polypeptides canced by the markers, antibodies that selectively bind to the college to developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antibense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer sample. A difference between the a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the carriersponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker corresponding to the marker. The presence of protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker or anneals with a portion of the marker is assessed by detecting the marker or anneals with a portion of the polymucleotide comprising the marker or anneals with a portion of the polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide which anneals with the marker or anneals with a subsequent the sample at a first point in time, repeating the method is carried out time and comparing the level of expression. The method is carried out sample at a first point in time, repeating the method is carried out the printed appearance represents a human ovarian cancer DNA marker of the printed appearance represents a human ovarian cancer in a print did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                       Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the printed specification, but was obtained in electro
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 9991; 106pp; English.
                                                                                                                                                                                                                                                                    2000US-0207124P.
2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
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                                                                                                             WO200170979-A2
                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                         25-MAY-2000;
15-JUN-2000;
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25-JUL-2000;
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                                                                                                                                                          27-SEP-2001
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Gaps ö DB 5; Length 310; 0; Indels Seguence 310 BP; 72 A; 54 C; 66 G; 118 T; 0 U; 0 Other; 100.0%; Pred. No. Score 24; 24; Conservative Local Similarity Query Match Best Loca Matches

1690 TAAGTACCTCGGCCGCGACCACGC 1713 30 raagraccredecedeceacea

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian calcs. The invention also relates to polypeptides canced by the markers, antibodies that selectively bind to the canced by the markers antibodies that selectively bind to the patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclecide complementary to a marker of the invention. The markers are useful for assessing the level of expression of the amarker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the carriersponds to a secreted protein or to a transcribed of polynuclectide or its portion. The level of expression of the marker corresponding to the marker. The level of expression of the marker corresponding to the marker. The presence of protein or protein cragment corresponding to the marker. The presence of protein or protein cragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker. The presence of a transcribed the marker is assessed by detecting the marker or anneals with a portion of the polymuclectide comprising the marker or anneals with a portion of the polymuclectide comprising the marker or anneals with a patient content which involves detecting the progression of the marker is also used for monitoring the progression of the marker is a patient sample at a first point in time, repeating the method is carried out time and comparing the level of expression. The marker is a patient sample at a first point in time, repeating the method of crast ovarian cancer. This sequence represents a human ovarian cancer plant of the printed specifi
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                                                                                                                                                                          Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 10381; 106pp; English,
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                                                                                                                              Human ovarian cancer DNA marker #10381
                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0207124P.
2000US-0211940P.
2000US-0216820P.
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                                                                                                                                                                                                                     Homo sapiens.
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cancer
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ID ADI7
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                                                                                                                                                                         Gaps
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                                                       Seguence 312 BP; 99 A; 53 C; 47 G; 113 T; 0 U; 0 Other;
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                            Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 1; Matches 24; Conservative 0; Mismatches
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                                                                                                                                                                                                                           1690 TAAGTACCTCGGCCGCGACCACGC 1713
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25-MAY-2000; 2000US-0207124P.
15-UIN-2000; 2000US-0211840P.
07-UUL-2000; 2000US-0216820P.
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21-DEC-2000; 2000US-0257672P.
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ADI71332 standard; DNA; 312
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the polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypoptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention.
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100.0%; Pred. No. 1;
...ive 0; Mismatches
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2000US-0211940P.
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2000US-0220661P.
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Best Local Similarity 100.0
Matches 24; Conservative
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expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein cragment corresponding to the marker. The presence of protein or protein cragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed to polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient cample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, the properties or antibody of the invention is used to treat ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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100.0%; Pred. No. 1;
tive 0; Mismatches 0; Indels
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Z1-MAR-2000; 2000US-0191031P.
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Z1-MAR-2000; 2000US-020124P.
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Z1-MAR-2000; 2000US-020124P.
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Z1-MAR-2000; 2000US-021630P.
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Z1-MAR-2000; 2000US-021630P.
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Novel isolated nucleic acid moper cancer cells as compared to the pr
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2000US-0216820P.
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concoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a patient sample and a normal level of expression of the carker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of the capters of portion or protein cancer in a patient sample and a normal level of expression of the capters of polymucleotide or its portion. The level of expression of a sasessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed or the polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide which anneals with the marker, under stringent conditions. The patient which involves detecting expression of the marker in a patient of patient which involves detecting expression of the marker in a patient or sample at a first point in time, repeating the method at a subsequent cime and comparing the level of expression comparian cancer. Or using an ovarian tissue sample. A composition comprising a marker. The sequence data for this patent did not form part of the printed specification, where the printed specification, where the printed specification, where the printed specif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, colon cancer; cancer; tissue profiling; forensic; mapping;
genetic analysis; diagnostic; antisense therapy; gene; 88.
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from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 1;
ative 0; Mismatches
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Best Local Similarity 100.
Matches 24; Conservative
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Thiaglingam A, Lewis ME;
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covarian cancer cells as compared to their expression in normal (i.e. noncacous) ovarian cells. The invention also relates to polypeptides encoded by the marker, antibodies that selectively bind to the cenceded by the marker, antibodies that selectively bind to the cenced by the marker of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of the carrier corresponding to the level of expression of the capturelectide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide of or monitoring the presence of a transcribed out time and comparing the level of expression of the marker is a busequent to a patient which involves detecting the marker, under stringent conditions. The manker is and comparing the level of expression of the marker in a patient warment at a first point in time, repeating the method is carried out time and comparing the level of expression. The method is carried out time and comparing the level of expression comparising the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the printed appearance of the printed appearanc
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100.0%; Pred. No. 1.
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2000US-0189315P.

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2000US-0210600P.
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ID AAH69655 standard; cDNA; 331
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                                                                                                 ABQ563106 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60775 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoractive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of colon cancer in a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
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              or
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      tissues useful for determining the presence of colon cancer in a cell tissue type, and in antisense therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Length 320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 320 BP; 66 A; 89 C; 89 G; 75 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; bcc.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 TAAGTACCTCGGCCGCGACCACGC 312
                                                                 Claim 1; Fig 1; 796pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL44057 standard; DNA; 326 BP
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2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
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Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2000;
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AAH69708 standard; cDNA; 338
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14-MAR-2000; 2000US-0189315P-
12-MAY-2000; 2000US-0203791P-
09-JUN-2000; 2000US-0210600P-
21-JUL-2000; 2000US-0220114P-
                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-2000; 2000WO-US03312
                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0169681P
                                                                                                                                                                                                                                                        19-SEP-2001 (first entry)
                                                                                              24; Conservative
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ses 24; Conserv
                                                                                   Local Similarity
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Matches
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AAH69708/
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                                              New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                   cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a parealignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                        genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and
                                                                                                                                                                                                                                                                    Gaps
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1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human breast cancer expressed polynucleotide 5537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                    100.0%; Pred. No. 1;
tive 0; Mismatches
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 Zhao X;
                                                                                                                                                                                                                                           1.4%; Score 24;
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                                                                                Claim 1; Page 257-258; 1051pp; English
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 Berger A,
                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                        The invention relates to novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-025310P.
09-JUN-2000; 2000US-0211315P.
                                                                                                                                                                                                                                                                                                                                                                            AAL13080 standard; cDNA; 337
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                  Matches 24; Conservative
                                                                                                                                                                                             useful for gene therapy
 Deeds J,
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                     WPI; 2001-375006/39.
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Best Local Similarity
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 Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                                                                                   Gape
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                                                                                                                                                                                  DB 4; Length 337;
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Pred. No. 1;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   Indels
                                                                                                                        Sequence 337 BP; 127 A; 63 C; 60 G; 83 T; 0 U; 4 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cervical cancer marker nucleic acid 982.
                                                                                                                                                                                  1.4%; Score 24; DB
100.0%; Pred. No. 1;
:ive 0; Mismatches
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100.08; Pre-
0; }
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Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

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                                                                                                      Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of
                                                                                                                                                                                                                                                                                                                                                                           prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
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                                                                                 Human prostate expression marker cDNA 7995
                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                        Monahan JE;
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      ABV08004/c
ID ABV08004 standard; cDNA; 346 BP.
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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                                                                                                                                                                                                                                                                              2000US-0255281P
                                                            (first entry)
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Best Local Similarity 100.
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                             WPI; 2001-662795/76.
                                                                                                                                                          WO200160860-A2
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09-JUN-2000;
18-JUL-2000;
                                                                                                                                       Homo sapiens.
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                                                             13-SEP-2002
                                                                                                                                                                                                                                     L6-MAR-2000;
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                                         ABV08004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 53
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70

Lillie J;

Lee J,

21-DEC-2000; 2000US-0257672P

07-JUL-2000; 25-JUL-2000; 15-JUN-2000; 21-MAR-2000; 25-MAY-2000;

; 2000US-0191031P. ; 2000US-0207124P. ; 2000US-0211940P. ; 2000US-0216820P. ; 2000US-0226661P.

21-MAR-2001; 2001WO-US009126.

WO200170979-A2. Homo sapiens.

27-SEP-2001

Disclosure; SEQ ID NO 11010; 106pp; English

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian calls. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the cancerous) ovarian cancer involving inhibiting expression of a gene or of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer involving inhibiting expression of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker or sepaponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the protein fragment. Alternatively, the level of expression of the protein fragment is assessed by detecting the marker or anneals with a portion of the polynucleotide which anneals with the marker or anneals with a patient sample at a first point in time, repeating the marker in a patient sample at a first point in time, repeating the method at a subsequent using an ovarian tissue sample. A composition comprising a marker or in a patient which involves detecting the presence of the marker or a patient which involves detecting the encode of the marker or anneals with a polynerial comparing the encode of the marker or anneals with a patient which involves detecting the comparing the marker or anneals with a patient sample at a first point in time, repeating the marker or a 
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Human ovarian cancer DNA marker #11010.

(first entry)

20-MAY-2004

ADL37120;

Sequence 368 BP; 96 A; 67 C; 84 G; 120 T; 0 U; 1 Other;

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncancerus) ovarian calls. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the encoded by the markers intribodies that selectively bind to the corresponding to a marker of the invention and a method of inhibiting ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonucleotide complementary to a marker of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a separession levels indicates ovarian cancer ample. A difference between the corresponding to the marker. The presence of protein or protein cancer in a sessessed by detecting the presence in the sample, a protein or protein cancer in a sessessed by detecting the presence of a transcribed comparing to the marker. The presence of a transcribed complexed by detecting the marker or anneals with the marker is also used for monitoring the presence of the marker in a patient contained and comparing the method at subsequent contained out the marker is also used for monitoring the method at subsequent contained out the marker is an encoded of the marker of the marker is also used for monitoring the method at subsequent contained by the propersion of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
                                                                                                                                                                                                                                                                                                                                                                                                Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                             Human ovarian cancer DNA marker #4711.
ADI71969 standard; DNA; 368 BP.
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2000US-0211940P.
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                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                             ADI71969;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                 Gaps
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    Length 368;
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                                               Indels
  1.4%; Score 24; DB 5;
100.0%; Pred. No. 1;
tive 0; Mismatches
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                                                                                     1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                        Human ovarian cancer DNA marker #5958.
                                                                                                             30 TAAGTACCTCGGCCGCGACCACGC 7
                                                                                                                                                                                                                                ADI73216 standard; DNA; 370 BP
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2000US-0211940P.
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                                               24; Conservative
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee J, Lillie J;
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25-JUL-2000;
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marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                               1.4%; Score 24; DB 5; Length 370; 100.0%; Pred. No. 1; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                               Sequence 370 BP; 131 A; 76 C; 61 G; 96 T; 0 U; 6 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian cancer DNA marker #12238
                                                                                                                                                                                                                                                                                            1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                      30 TAAGTACCTCGGCCGCGACCACGC 7
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2000US-0211940P.
2000US-0216820P.
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21-DEC-2000; 2000US-0257672P.
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                     Similarity
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                                                                                                                                             invention
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Best Local 8
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consider corresponds to a secreted protein or to a transcribed polymucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of protein or protein fragment. Alternatively, the level of expression of merker is assessed by detecting the presence of a transcribed polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for detecting presence of prostate cancer, stage of prostate cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                           Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                     Sequence 370 BP; 131 A; 76 C; 61 G; 96 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate expression marker cDNA 6066.
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 TAAGTACCTCGGCGCGACCACGC 7
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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Best Local Similarity 100.
Matches 24; Conservative
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                       invention.
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progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a
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                                                                                                                                                                               Sequence 376 BP; 122 A; 55 C; 63 G; 136 T; 0 U; 0 Other;
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Pred. No.
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15-JUN-2000;
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marker corresponds to a secreted protein or to a transcribed

polynucleotide or its portion. The level of expression of the marker is

sasessed by detecting the presence in the sample, a protein or protein

fragment corresponding to the marker. The presence of protein or protein

fragment corresponding to the marker. The presence of protein or protein

fragment is detected using an antibody that specifically binds with the

critical or protein fragment. Alternatively, the level of expression of

the marker is assessed by detecting the presence of a transcribed

condition or protein fragment. Alternatively, the level of expression of

the marker is assessed by detecting the presence of a transcribed

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conditions of a transcribed portion of

conditions or patient which involves detecting the marker of varian cancer in a

condition of patient which involves detecting expression of the marker in a patient

condition of the level of expression. The method is carried out

cuing an ovarian tissue sample. A composition comprising a marker.

condition or antibody of the invention is used to treat ovarian cancer.

conditions or antibody of the invention is used to treat ovarian cancer.

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conditions or antibody of the invention cancer on the printed specification, but was obtained 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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WPI; 2001-611502/70.

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corcoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonuclecide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker orresponds to a secreted protein or to a transcribed polynuclectide or its portion. The level of expression of a secreted protein or to a transcribed polynuclectide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is a sasessed by detecting the presence of a transcribed polynuclectide which anneals with the marker or anneals with a portion of the polynuclectide which anneals with the marker or anneals with a portion of the polynuclectide comprisain the marker or anneals with a portion of the polynuclectide which anneals with the marker in a patient sample at a first point in time, respecting the marker in a subsequent cancer in a service and comparing the level of expression. The marker is a subsequent cancer in a patient sample at a first point in time, respecting the marker or anneals of the marker or in a patient cancer in a subsequent cancer in a cancer in a 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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tive 0; Mismatches 0; Indels
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from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concernation ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclectide complementary to a marker of the patient an antisense oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of with ovarian cancer, which involves comparing the level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a sested by detecting the presence in the sample, a protein or protein cancer is detected using an antibody that specifically binds with the protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment is assessed by detecting the presence of a transcribed comprising the presence of a transcribed comprising the presence of a transcribed comprising the presence of a variant contein of the marker is assessed by detecting the presence of a variant contein of the marker is an antibody that specifically binds with the marker in a marker in a portion of the marker is a sessed by detecting the presence of a variant contein or protein or protein fragment is also most of a marker or anneals with the marker in a marker in a serial or protein or protein or protein defined comprising the progression of continuous cancer in a marker is a serial or protein defined or such a protein or protein or pro
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                                              Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are
                                                                                                     used to characterize stage, grade, histological type of ovarian cancer.
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ID ADL42485 standard; DNA; 391
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Best Local S
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                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concerous) ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a the patient antibense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a patient sample and a normal level of expression of the expression never in a control non-ovarian cancer. The level of expression of a marker in a control non-ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed cor its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is a sessessed by detecting the presence of protein or protein corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is a sessessed by detecting the presence of protein or protein or protein corresponding to the marker. The presence of protein or protein corresponding to the marker. The presence of protein or protein o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method at subsequent using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a human ovarian cancer DNA marker of the monthly invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                   Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 391 BP; 90 A; 74 C; 90 G; 137 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 16375; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 1;
tive 0; Mismatches
                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
21-JUL-2000; 2000US-0250661P.
21-DEC-2000; 2000US-0257672P.
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                                                                                                                                                                                 WPI; 2001-611502/70.
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Best Local Similarity
                                                                                                                                         Lillie J;
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                                                                                                                                         Lee J,
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70.

Lee J, Lillie J;

2000US-0216820P

07-JUL-2000; 15-JUN-2000; 25-MAY-2000;

21-DEC-2000; 2000US-0257672P

21-MAR-2001; 2001WO-US009126

21-MAR-2000;

WO200170979-A2 Homo sapiens.

27-SEP-2001

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancercous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of a marker in a patient sample and a normal level of expression of the invention. The marker in a patient sample and a normal level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker ortesponds to a secreted protein or a transcribed polymucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the polymucleotide which anneals with the marker or a marker is also used for monitoring the presence of a transcribed polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide comprising the marker, under stringent conditions. The sample at a first point in time, repeating the method as a subsequent using an ovarian tissue sample. A composition comprising a marker or anneals with a sequence represent or the method is carried out using an ovarian tissue sample. A composition comprising a marker of the invention is used to transcribed or antibody of the invention is used to transcribed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 392 BP; 115 A; 50 C; 78 G; 146 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%; Score 24; DB
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Disclosure; SEQ ID NO 9592; 106pp; English
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Matches 24; Conserv
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RESULT 63 ADI70525/c

Gaps

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Length 392; 0; Indels

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DB

WO200170979-A2 Homo sapiens.

27-SEP-2001

20-MAY-2004

ADI70525

21-MAR-2000;

Lee J,

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specificaction or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker; gene, ss.
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                              100.0%; Pred. No. 1; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate expression marker cDNA 8043.
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      1.4%; Score 24;
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                                                                                                                      1690 TAAGTACCTCGGCGCGCACCACGC 1713
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                                                                                                                                                    30 TAAGTACCTCGGCCGCGACCACGC 7
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09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
                                                                                                                                                                                                                                                                                                                           ABV08052 standard; cDNA; 404
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                                                            24; Conservative
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les 24; Conserv
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     ABV08052;
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Matches
                                                                                                                                                                                                                                                                  RESULT 64
ABV08052/c
                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncovarian cancer cells as compared to their expression in normal (i.e. noncovarian cancer) ovarian calls. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the corresponding to a marker of the invention and a method of traating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a convertion. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a control non-ovarian cancer sample. A difference between the capression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed captorial indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comprising the marker or anneals with a portion of the polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide comprising the marker or anneals with a portion of patient which involves detecting expression of the marker is also used for monitoring the presence of a transcribed caption and comparing the level of expression. The method at a subsequent cime and comparing the level of expression of the marker is also used for monitoring the presence of a transcribed captor marker is also used for monitoring the presence of a transcribed out time and comparing the level of expression. The method is carried out time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at frp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                      Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3267; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                Human ovarian cancer DNA marker #3267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2000; 2000US-0207124P.
15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
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   ADI70525 standard; DNA; 392
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DB 5; Length 404;

Sequence 409 BP; 124 A; 85 C; 90 G; 110 T; 0 U; 0 Other;

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The invention relates to nucleic acid markers which are overexpressed in caracraus) ovarian calls as compared to their expression in normal (i.e. noncaracraus) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient afflicted with ovarian cancer comprising the level of expression of invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of the marker in a patient sample and a normal level of expression of the expression nevels indicates ovarian cancer. The level of expression of the marker in a control non-ovarian cancer mapple. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed protein or protein cansers assessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the fragment is detected using an antibody that specifically binds with the fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is also used for monitoring the presence of a transcribed polymuclectide which anneals with the marker or anneals with a pottion of the polymuclectide which anneals with the marker or anneals with a patient or apatient which involves detecting expression of the marker is also used for monitoring the progression of ovarian cancer in apatient which involves detecting expression of the marker of the point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out this sequ
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                                                                                                                                                                      Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                           Human ovarian cancer DNA marker #16049.
ADL42159 standard; DNA; 409 BP
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25-JUL-2000; 2000US-0220661P.
21-DEC-2000; 2000US-0257672P.
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2000US-0211940P.
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                                                                              (first entry)
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15-JUN-2000;
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                                          ADL42159;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncace cancervous) ovarian cells. The invention also relates to polypeptides cancervous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient afflicted with ovarian cancer comprising providing to cells of the patient afflicted with ovarian cancer comparing if a patient is afflicted with ovarian cancer. Which involves comparing the level of expression of the markers are useful for assessing if a patient is afflicted with ovarian cancer. Which involves comparing the level of expression of the carriers in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a carrier corresponds to a secreted procein or to a transcribed polynucleotide or its portion. The level of expression of a cassessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the corresponding the presence of a transcribed comparised by detecting the presence of a transcribed comparised by the marker or anneals with a portion of the polynucleotide which anneals with the marker, under stringent conditions. The
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5; Length 409;
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Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 1; Matches 24; Conservative 0; Mismatches
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                                                                              1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                          ADL43269 standard; DNA; 415 BP
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25-JUL-2000;
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marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 1;
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Matches 24; Conservative
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compares in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed compares of the marker is assessed by detecting the presence in the sample, a protein or protein cragment corresponding to the marker. The presence of protein or protein cragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide which anneals with the marker or anneals with a portion of compression of the progression of covarian cancer in a patient which involves detecting expression of the marker in a patient comparing the level of expression of the marker in a patient consisting an ovarian tissue sample. A composition comprising a marker, but an experience represents a human ovarian cancer DNA marker of the constraint cancer.
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tive 0; Mismatches
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ADI72479/c
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cc encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of a marker in a patient sample and a normal level of expression of the carbers in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker orresponds to a secreted protein or a transcribed corresponds to a secreted protein or a transcribed polymucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment orresponding to the marker. The presence of a transcribed corresponding to the marker. The presence of a transcribed corporation or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed copulanceotide which anneals with the marker or ameals with a portion of the polymucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the presence of a transcribed comprising the marker, under stringent conditions. The patient which involves detecting expression of the marker in a patient companing and comparing the level of expression of the marker in a patient condition and comparing the level of expression of the marker or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer in a patient when the sequence represents a human ovarian cancer. The marker is an experience and the sequence represents a human ovarian cancer. The marker is an experience and in the apprentice of the antibody of the invention is parent for the antibody of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 69
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian calcs. The invention also relates to polypeptides canceded by the markers, antibodies that selectively bind to the canceded by the markers, antibodies that selectively bind to the patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer sumple. A difference between the amarker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed corresponds to a secreted protein or to a transcribed oplynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker, under stringent conditions. The marker is assessed by detecting the marker, under stringent conditions. The marker is assessed by detecting the marker, under stringent conditions. The marker is assessed by detecting the marker, under stringent conditions. The marker is a sion used for monitoring the progression of fovarian cancer in a polymoclectide comprising the marker, under stringent conditions. The manple at a first point in time, repeating the method is carried out time and comparing the level of expression of the marker in a subsequent cuing an ovarian tissue sample A composition comprising a new part of invention. Note: The sequence data for this patent data of the printed of partication. T
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                                         Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 420 BP; 126 A; 77 C; 77 G; 140 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                  Disclosure; SEQ ID NO 12779; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%; Pred. No. 1; tes 24; Conservative 0; Mismatches
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Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                        cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer
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                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                       2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
                    2000US-0207124P
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Best Local Similarity
                                                                                                                                                                                              Lee J, Lillie J;
                                         15-JUN-2000;
07-JUL-2000;
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                    25-MAY-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cells. The invention also relates to polypeptides canceded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclecide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer semple. A difference between the amarker in a control non-ovarian cancer sample. A difference between the amarker in a control non-ovarian cancer sample. A difference between the marker corresponds to a secreted protein or to a transcribed of copyunclectide or its portion. The level of expression of the marker corresponding to the marker. The level of expression of the assessed by detecting the presence in the sample, a protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is also used for monitoring the presence of a transcribed of the polymuclectide which anneals with the marker or anneals with a portion of the polymuclectide which anneals with the marker or anneals with a patient comprising the level of expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method at a subsequent cuing an ovarian tissue sample. A composition comprising a marker of the prince of protein or protein and a first point in time, repeating the method is carried out the prince appeared a pecification, but was obstanced in electronic format direction. This sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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Pred. No.
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2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
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                                                                                                                                                                                                                            21-MAR-2001; 2001WO-US009126
                                                                                                                                                                                                                                                                                                         2000US-0191031P
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                                                                        WO200170979-A2.
Homo sapiens.
                                                                                                                                                                                                                                                                                                         21-MAR-2000;
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ABV39230/

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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleocide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                 Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 1;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 7580; 36pp; English.
                       Breast cancer related marker, seg id 7580.
                                                                                                                                                                                                                                                                                                                                                                               Xu Y, Wang Y, Steinmann K;
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                                                                                                                                                                                                                                                                                         18-JUL-2001; 2001US-0306220P.
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                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2001; 2001WO-US005171
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                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                             Lillie J,
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Matches
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                                                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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1;
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                                                                                                                                                                                                                        Human prostate expression marker cDNA 39221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monahan JE;
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                                                                                      ABV39230 standard; cDNA; 424 BP.
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2000US-0207454P.
2000US-0211314P.
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ID ACN86430 standard; DNA; 425
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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25-MAY-2000;
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RESULT 73

ACN86430

Query Match

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WPI; 2001-611502/70.
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                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h)
                                                                                                                                                                                                                                                                                                                       assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 5; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                          Sequence 426 BP; 116 A; 102 C; 110 G; 98 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ...
                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                           1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ovarian cancer DNA marker #18496.
                                                                                                                                                                                   Claim 1; Page 1075; 11750pp; English.
                                                                                          Monahan JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            30 TAAGTACCTCGGCCGCGACCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL44606 standard; DNA; 426 BP
           ; 2000US-0207454P.
; 2000US-0211314P.
; 2000US-0219007P.
; 2000US-0255281P.
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2000US-0216820P.
2000US-0220661P.
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                                                                                         Schlegel R, Endege WO,
                                                                                                                 WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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16-MAR-2000; 25-MAY-2000; 209-JUN-2000; 2
                                   18-JUL-2000;
                                              13-DEC-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncac cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the corresponding to the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a control non-ovarian cancer. The level of expression of the capression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed capterestory detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed corresponding to marker. The presence of a transcribed corresponding to marker under stringent conditions. The protein or protein fragment. Alternatively, the level of expression of the marker is also used for monitoring the presence of a transcribed corresponds which anneals with the marker or anneals with a patient or patient which involves detecting expression of the marker is also used for monitoring the progression of the marker is also used for monitoring the presence of a transcribed out conditions and comparing the level of expression of the marker is also used for monitoring the marker in the marker is also used for monitoring the marker in the marker is an expectatio
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                                cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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   ovarian
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Novel isolated nucleic acid molecules (markers) overexpressed in cancer cells as compared to their normal non-cancerous ovarian ce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ore 24; DB 5;
red. No. 1;
Mismatches 0
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                                                                                                                                         Disclosure; SEQ ID NO 18496; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; Score 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1690 TAAGTACCTCGGCGCGCGACCACGC 1713
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100.0%; Fr.
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Best Local Similarity 100.
Matches 24; Conservative
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21-MAR-2000; 2000US-0191031P.
25-MAY-2000; 2000US-0207124P.
WPI; 2001-611502/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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Matches
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                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h)
                                                                                                                                                                                                                                                                                                      assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of
                                                                                                                                       prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 432;
1;
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                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                     Sequence 432 BP; 153 A; 67 C; 75 G; 137 T; 0 U; 0 Other;
                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                         ch 1.4%; Score 24; DB 1.8 Similarity 100.0%; Pred. No. 1; 24; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ovarian cancer DNA marker #18622.
                                                                                                                                                                                                                                                                                                                                                                                                     1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                       Claim 1; Page 7755; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  TAAGTACCTCGGCCGCGACCACGC 33
                                                                                    Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL44732 standard; DNA; 432 BP.
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2000US-0216820P.
2000US-0220661P.
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                    2000US-0211314P
                               2000US-0219007P
                                         13-DEC-2000; 2000US-0255281P.
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                                                                                    Endege WO,
                                                                                                       WPI; 2001-662795/76
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Best Local Similarity
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                    09-JUN-2000;
                               18-JUL-2000;
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                                                                                  Schlegel R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL44732;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian calls. The invention also relates to polypeptides cancerous) ovarian cancer antibodies that a selectively bind to the cancerous) ovarian cancer intolving expression of a gene corresponding ovarian cancer involving inhibiting expression of a gene corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer involving inhibiting providing to cells of the patient an antisense oligonucleotide complementary to a marker of the patient an antisense oligonucleotide complementary to a marker of a marker in a patient sample and a normal level of expression of the invention. The marker is a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A duifference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed comprised by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the protein or protein fragment. Alternatively, the level of expression of the patient which involves detecting the presence of a transcribed comprising the antibody that specifically binds with a portion of the patient which involves detecting expression of the marker in a patient comprising the level of expression of the marker in a patient which involves detecting expression of the marker in a patient which involves detecting expression of the marker in a patient which involves detecting the presence of a transcribed or marker is also used for monitoring the presence of 
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                Disclosure; SEQ ID NO 18622; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Score 24; DB 100.0%; Pred. No. 1; ive 0; Mismatches
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the cancerous) ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the invention. The patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is a ssessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide which anneals with the marker is also used for monitoring the presence of a transcribed polynucleotide which anneals with the marker is a subsequent conditions. The marker is also used for monitoring the presence of a transcribed patient which involves detecting expression of the marker is a subsequent or expression of the marker in a patient which involves detecting expression of the marker in a patient which involves detecting expression or in the subsequent contains an integral or expression or in the sample at a 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide or antibody of the invention is used to treat ovarian cancer. sequence represents a human ovarian cancer DNA marker of the
                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3100; 106pp; English
                           2000US-0216820P
                                                       25-JUL-2000; 2000US-0220661P.
21-DEC-2000; 2000US-0257672P.
                                                                                                                                                                                                                                                                  WPI; 2001-611502/70.
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1.4%; Score 24; DB 5; Length 437;
100.0%; Pred. No. 1;
ive 0; Mismatches 0; Indels
                                                    1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                            Conservative
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Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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AD176684/C
ID AD176684 standard; DNA; 437 BP
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Human; ovarian cancer; ds; tum
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OS Homo sapiens.
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ADL44126 standard; DNA; 442 BP

ADL44126/c ID ADL44 XX RESULT 80

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the conceded by the markers in involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonucleotide complementary to a marker of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer useful for assessing if a patient is afflicted with ovarian cancer useful for assessing if a patient is afflicted with ovarian cancer sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed cassessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of protein or protein corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein cancer she marker is a sesses of by detecting the presence of protein or protein cancer the marker is a sesses of by detecting the presence of protein or protein cancer the marker is a sesses of by detecting the presence of protein or protein cancer when the marker is a sesses of by detecting the presence of protein or protein cancer when the marker is a sesses of by detecting the presence of protein or protein cancer when the marker is a protein or prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 9426; 106pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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15-UIN-2000; 2000US-0211940P.
07-UIL-2000; 2000US-0216920P.
25-UIL-2000; 2000US-025064EP.
21-DEC-2000; 2000US-0257672P.
                                                                                                                                            21-MAR-2001; 2001WO-US009126
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                        WO200170979-A2.
                                                                                  27-SEP-2001
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1690 TAAGTACCTCGGCCGCGACCACGC 1713

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian calls. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concernation of a gene corresponding to a marker of the invention and a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antilense oligonucleotide comprising providing to cells of invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a control non-ovarian cancer. The level of expression of the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of protein or protein croresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian an experience of the polynucleotide comprising the progression of a marker in a marker is a second to a marker. The presence of a transcribed polynucleotide which anneals with the marker, under stringent conditions. The marker is also used for monitoring the progression of a presence in a marker is a second to a marker or anneals with a portion or protein and a polynucleotide comprising the progression of a presence of a presence of a presence of a presence of a p
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                                                                                                                                                                                                                                                                                                                           Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                Human ovarian cancer DNA marker #18016.
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25-MAY-2000; 2000US-0207124P.
15-JUN-2000; 2000US-0211940P.
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25-JUL-2000; 2000US-0220661P.
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This sequence represents a
                                                                                                          20-MAY-2004 (first entry)
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ADL44126;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerums) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers artibodies that selectively bind to the corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to calls of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the amarker in a control non-ovarian cancer. The level of expression of the capression lavels indicates ovarian cancer. The level of expression of a capter corresponds to a secreted protein or to a transcribed capted or its portion. The level of expression of the marker corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment is assessed by detecting the presence of a transcribed correction correction correction correction or protein fragment is assessed by detecting the presence of a transcribed correction correction correction correction or protein fragment is assessed by detecting the presence of a transcribed correction or protein fragment is assessed by detecting the presence of a transcribed correction or protein fragment is assessed by detecting the presence of a transcribed correction or protein fragment is assessed by detecting the presence of a transcribed correction or protein fragment is assessed by detecting the marker is assessed by detecting the marker is an antipody that presence of a transcribed continuation of the polynucleotide which anneals with the marker is an animal for monitoring the presence or anneals with a portion or pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                  Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 15845; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                  Human ovarian cancer DNA marker #15845.
               83
106 TAAGTACCTCGGCCGCGACCACGC
                                                                                                                                             ADL41955 standard; DNA; 444 BP
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2000US-0211940P.
2000US-0216820P.
2000US-0220661P.
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                                                                                                                                                                                                                                             20-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee J, Lillie J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200170979-A2
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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15-JUN-2000;
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25-JUL-2000;
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                                                                                                                                                                                             ADL41955;
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ID ADL4:
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Gaps

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Query Match
1.4%; Score 24; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels

Gaps

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Indels

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Mismatches

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24;

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1690 TAAGTACCTCGGCCGCGACCACGC 1713
Matches
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          invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                   cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                            Gaps
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cancer DNA marker of the
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                                                                                 DB 5; Length 444;
1;
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1;
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                                                          Sequence 444 BP; 152 A; 77 C; 116 G; 99 T; 0 U; 0 Other;
                                   from WIPO at ftp.wipo.int/pub/published pct sequences.
                                                                           1.4%; Scc...
100.0%; Pred. No. .,
... 0; Mismatches
                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 36032.
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This sequence represents a human ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4%; Score 24;
100.0%; Pred. No.
                                                                                                                                  1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                         73 TAAGTACCTCGGCGCGCGACCACGC
                                                                                                                                                                                                           ABV36041/c
ID ABV36041 Btandard; cDNA; 446
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2000US-0207454P.
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2000US-0219007P.
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                                                                                                                                                                                                                                                                       (first entry)
                                                                                                            24; Conservative
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Best Local Similarity
                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                       Human; prostate
pharmacogenomic
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18-JUL-2000;
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25-MAY-2000;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 37963.
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                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 7762; 11750pp; English.
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101 TAAGTACCTCGGCCGCGACCACGC
                                                                                                                                                                   BP.
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                                                                                                                     ABV37972/c
ID ABV37972 standard; çDNA; 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200160860-A2.
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09-JUN-2000;
18-JUL-2000;
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ABV45101/c

2000US-0207124P. 2000US-0211940P. 2000US-0216820P.

2000US-0191031P.

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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 10610; 106pp; English
                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                   21-MAR-2001; 2001WO-US009126.
                                                                                                                                                           25-JUL-2000; 2000US-0220661P
21-DEC-2000; 2000US-0257672P
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                                                                                                                                                                                                                       Lee J, Lillie J;
                                     WO200170979-A2
              Homo sapiens.
                                                                                                                                  15-JUN-2000;
07-JUL-2000;
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                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 446 BP; 137 A; 71 C; 85 G; 153 T; 0 U; 0 Other;
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                                                                         Human prostate expression marker cDNA 45092.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 8933; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                Monahan JE;
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ABV45101 standard; cDNA; 446 BP
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25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-021314P.
18-JUL-2000; 2000US-0219007P.
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Best Local Similarity 100...
Best Local Standards 100...
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                                                16-SEP-2002
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                        ABV45101;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian calls. The invention also relates to polypeptides cancerous) ovarian cancer antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the corresponding ovarian cancer involving inhibiting expression of a gene corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonuclectide complementary to a marker of the patient as male large comparing the level of expression of the invention. The marker in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of the marker in a patient and expression cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a genessed by detecting the presence of expression of the marker is assessed by detecting the presence of expression of the marker is a sessessed by detecting the presence of expression of the protein or protein fragment. Alternatively, the level of expression of the patient as assessed by detecting the presence of a transcribed polymucleotide which anneals with the marker, under stringent conditions. The marker is also used for monitoring the presence of a transcribed patient which involves detecting expression of the marker in a patient cancer in a patient which involves detecting expression of the marker in a patient cancer in a patient which involves detecting the presence of a transcribed compariant shall be level of expression of the marker is also used for monitoring the presence of a transcribed contain and compariant the marker is expensively of the invention is used to treat ovarian cancer in a patient which involves detecting expression of the marker is also us
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Matches 24; Conserv
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Human; ovarian cancer; d8; tumour; cytostatic; DNA marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                                                                                     Human ovarian cancer DNA marker #4306.
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15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
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21-DEC-2000; 2000US-0257672P.
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ADI71564 standard; DNA; 446
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1.4%; Score 24; DB 5; Length 446; 100.0%; Pred. No. 1;

Query Match Best Local Similarity

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Human, nootropic, neuroprotective, cytostatic, dermatological, virucide, immunosuppressive, antinflammatory, anti-HIV; antibacterial, vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebropective, antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
                                                                                                                                 Human nervous system related polynucleotide SEQ ID NO 135.
1690 TAAGTACCTCGGCGCGCGACCACGC 1713
           30 TAAGTACCTCGGCCGCGACCACGC
                                                                     ВP
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2000US-0218290P.
2000US-0220963P.
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2000US-0225270P.
2000US-0225447P.
                                                                    ABA11128 standard; cDNA; 449
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2000US-0225267P.
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                                                                                                            (first entry)
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                                                                                        ABA11128;
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                                                           ABA11128/
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2000US-0229513P.
2000US-0239437P.
2000US-0230437P.
2000US-0231242P.
2000US-0231244P.
2000US-0231414P.
2000US-0231414P.
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2000US-0231414P.
2000US-0232391P.
2000US-0232397P.
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2000US-023364DP
2000US-0233064P
2000US-0233065P
2000US-023423P
2000US-023423P
2000US-023429P
2000US-023499B
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2000US-0249207P.
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 05-SEP-2000; 205-SEP-2000; 206-SEP-2000; 206-SEP-2000; 208-SEP-2000; 208
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02-0CT-2000)
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02-OCT-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing (e) cardiovascular disorders such as myocardial ischaemias; (d) wound healing infectious diseases e.g. cerebral anoxia and epilepsy; and (f) infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
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Local Similarity 100.0%; Pred. No. 1;
es 24; Conservative 0; Mismatches
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                          2000US-0249244P
2000US-0249244P
2000US-0249264P
2000US-024929P
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ABQ75327 standard; cDNA; 457
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2000US-0251868P.
2000US-0251869P.
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2000US-0254097P
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P-PSDB; ABB14802.
                          17-NOV-2000;
17-NOV-2000;
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01-DEC-2000;
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11-DEC-2000;
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05-NOV-2002 (first entry)

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The present invention describes an isolated lung specific nucleic acid (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid sequences comprising 17 - 733 amino acids, given in ABP22813 to ABP2285; (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), given in ABQ75262 to ABQ75376; (c) selectively hybridises to (a) or (b); or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific protein (LSP) sequences have cytostatic activity and can be used in gene therapy and vaccines. LSNAs and LSPs are useful for diagnosing and monitoring the presence and metastases of lung cancer in a patient. An entity in a specifically by inducing an immune response against the vith lung cancer, particularly by inducing an immune response against the lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs and LSPs are useful for identifying, diagnosing, monitoring, staging, inaging and treating lung cancer (e.g. squamous cell carcinoma) and noncarcous disease states in lung
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                                                                                                                                                                                                                                                                                                                                                                                                             New lung specific nucleic acid useful in gene therapy or as vaccines for treating lung cancer (e.g. squamous cell carcinoma) or non-cancerous lung diseases, as well as for diagnosing, monitoring or staging these
                                                Human; lung; lung specific nucleic acid; LSNA; lung specific protein; LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer; squamous cell carcinoma; gene; chromosome 8; ss.
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              Human lung specific nucleic acid sequence SEQ ID NO:66.
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100.0%; Pred. No. 1;
+ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 186; 282pp; English.
                                                                                                                                                                                                                                                                                                                                           Chen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL44815 standard; DNA; 460 BP.
                                                                                                                                                                                                                                20-NOV-2001; 2001WO-US045080.
                                                                                                                                                                                                                                                                  20-NOV-2000; 2000US-0252054P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                                                                                                                                                                                                                                                                                                             Macina RA, Recipon H,
                                                                                                                                                                                                                                                                                                        (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-657601/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                           WO200264788-A2
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                                                                                                                           Homo sapiens.
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                                                                                                                                                                                               22-AUG-2002
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70. Lillie J;

Lee J,

2000US-0211940P.

25-MAY-2000; 15-JUN-2000; 07-JUL-2000; 25-JUL-2000:

21-MAR-2000;

2000US-0220661P

21-DEC-2000; 2000US-0257672P

21-MAR-2001; 2001WO-US009126

27-SEP-2001

Disclosure; SEQ ID NO 18705; 106pp; English

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerus) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers is antibodies that selectively bind to the conference of developing ovarian cancer involving inhibiting expression of a game corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the patient an antisense oligonucleotide complementary to a marker of the patient an antisense oligonucleotide complementary to a marker of the involves comparing the level of expression of with ovarian cancer, which involves comparing the level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker in a control non-ovarian cancer. The level of expression of a casceted protein or to a transcribed copyluucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein croves protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed correction or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comprising the marker. Under stringent conditions. The next or anneals with the marker or anneals with the marker or anneals with a portion of the marker is a sensesed by detecting the presence of a variant conditions. The narker is a senses of protein or protein or protein fragment is also used for monitoring the presence of a variant conditions. In a partion of the partion of the marker in a relient in a partion of the marker in a relient which anneals with the marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the printed specification, but was obtained in electro
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.0%; Pred. No. 1; 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24;
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70. Lee J, Lillie J;

25-MAY-2000; 2000US-0207124P.
15-UUN-2000; 2000US-0211940P.
07-UUL-2000; 2000US-0216820P.
25-UUL-2000; 2000US-0250661P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACNY881-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptide associated with breast cancer, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                      detecting presence of polypeptide in sample, as a marker for breast
                                                                                                     Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ....
                                                                     Breast cancer related marker, seq id 5501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 5501; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                  Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%; Score 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian cancer DNA marker #3344.
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ID AD170602/c

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AC AD170602;

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CO-MAY-2004 (first entry)

XX

DE Human ovarian cancer DNA marker #

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KW Human; ovarian cancer; ds; tumour

XX

KW W0200170979-A2.

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PD 27-SEP-2001.

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PP 21-MAR-2001; 2001WO-US009126.
                                                                                                                                                                                                                                                                                18-JUL-2001; 2001US-0306220P.
                                                                                                                                                                                                                                              18-JUL-2002; 2002US-00198846.
                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC.
                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-787014/74.
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                                                                                                                                                                                                                                                                                                                                                  Lillie J, Xu Y,
                                                                                                                                                                         US2003099974-A1.
                                                                                                                                          Homo sapiens.
                                  02-DEC-2004
                                                                                                                                                                                                           29-MAY-2003
 ACN84351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian calls. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concoded by the markers, antibodies that selectively bind to the corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves complementary to a marker of the corresponding to a secreted protein complementary to a marker of the with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynuclectide or its portion. The level of expression of the marker is assessed by detecting the presence of protein or protein fragment is detected using an antibody that specifically binds with the corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the polynuclectide omprising the marker or anneals with a portion of the polynuclectide omprising the marker or anneals with a portion of the patient which involves detecting the presence of protein or protein fragment. Alternatively, the level of expression of the marker is a subsequent of comprising the marker, under stringent conditions. The marker is also used for monitoring the presence of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression of the marker is also used for monitoring the presence of presence of presence of patient which involves detecting the presence arringent or animals with 
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100.0%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 3344; 106pp; English.
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Matches 24; Conservative
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Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

Human ovarian cancer DNA marker #15851.

20-MAY-2004 (first entry)

ADL41961;

ADL41961 standard; DNA; 471 BP

RESULT 93 ADL41961/

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerue) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the encoded by the markers antibodies that selectively bind to the triak of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the arker corresponds to a secreted protein or to a transcribed cappended or its portion. The level of expression of a marker corresponds to a secreted protein or to a transcribed or its portion. The level of expression of a sessessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the from or protein fragment is detected using the marker or anneals with a portion of the marker is assessed by detecting the presence of a transcribed collution of the marker is assessed by detecting the presence of a transcribed collution of the marker is assessed by detecting the marker or anneals with a portion of the polynucleotide which anneals with the marker is any or an anneals with a portion of a marker is a second for marker in an antibody that specifically binds with a portion of the polynucleotide which enemed to a marker in a partion of a marker is a sacreticed by the marker or anneals with a portion of a marker is a sacreticed by a marker is underly the marker is a marker is a sacretic anneals with the marker is a sacreticed by the marker or anneals with a portion of a marker is a sacreticed by the marker is a s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 9665; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                   25-MAY-2000; 2000US-0207124P.
15-JUN-2000; 2000US-0211940P.
07-JUL-2000; 2000US-0216820P.
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21-DEC-2000; 2000US-0257672P
                                                                                                                                                                                                                                 21-MAR-2001; 2001WO-US009126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611502/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lillie J;
                                                                                                                  WO200170979-A2
                                                               Homo sapiens.
                                                                                                                                                                           27-SEP-2001
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

WPI; 2001-611502/70. Lee J, Lillie J;

2000US-0257672P

21-DEC-2000; 07-JUL-2000; 25-JUL-2000;

2000US-0207124P. 2000US-0211940P. 2000US-0216820P. 2000US-0220661P.

21-MAR-2001; 2001WO-US009126

21-MAR-2000; 25-MAY-2000; 15-JUN-2000;

WO200170979-A2. Homo sapiens.

27-SEP-2001

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerus) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the corresponding to a marker of the invention and method of treating a corresponding to a marker of the invention and method of treating a corresponding to a marker of the invention and method of treating a corresponding to a marker of the invention and method of treating a corresponding to an arker of the patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the arker in a control non-ovarian cancer sample. A difference between the cappression levels indicates ovarian cancer. The level of expression of a corresponds to a secreed protein or to a transcribed cappends to a secreed protein or to a transcribed cappends to the marker. The level of expression of a capprotein or protein or protein fragment is detected using an antibody that specifically binds with the corresponding to the marker. The level of expression of the marker is assessed by detecting the presence of a transcribed coplynucleotide which anneals with the marker or anneals with a portion of marker is also need to marker in a partion of marker is a les used for monitoring the presence or anneals with a portion of marker is a les used for monitoring the presence or a protein or protein or protein fragment is also need to a marker in a portion of a marker is a les used for monitoring the marker is an anneals with a portion of a marker is a les used for monitoring the presence or a protein or prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 15851; 106pp; English.
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30 TAAGTACCTCGGCCGCGACCACGC 7

24; Conservative

Similarity

Local

Matches

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerus) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers artibodies that selectively bind to the encoded by the marker of the invention and method of treating a corresponding to a marker of the invention and method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of the capression levels indicates ovarian cancer. The level of expression of a casessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment is assessed by detecting the presence of a transcribed correct or polynucleotide which anneals with the marker or anneals with a portion of
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                                                                              Gaps
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                                       DB 5; Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
Sequence 471 BP; 132 A; 68 C; 104 G; 167 T; 0 U; 0 Other;
                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 10775; 106pp; English.
                                                    Best Local Similarity 100.0%; Pred. No. 1; Matches 24; Conservative 0; Mismatches
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                                       1.4%; Score 24;
                                                                                                                                                                                                                                                                                                                                                             Human ovarian cancer DNA marker #10775.
                                                                                                               1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                103 TAAGTACCTCGGCCGCGACCACGC 80
                                                                                                                                                                                                                                              ADL36885 standard; DNA; 486 BP
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15-UUM-2000; 2000US-0216820P.
07-UUM-2000; 2000US-0220661P.
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2000US-0207124P.
2000US-0211940P.
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                                     Query Match
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the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method at a subsequent using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to calls of the patient an antisense oligomoclecide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of
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                                                                                                                                                                                                                                                                            1.4%; Score 24; DB 5; Length 486; 100.0%; Pred. No. 1; 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                         Sequence 486 BP; 177 A; 69 C; 86 G; 135 T; 0 U; 19 Other;
                                                                                                                                                                                                 from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                            1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian cancer DNA marker #4472.
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                                                                                                                                                                                                                                                                                                                       24; Conservative
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25-MAY-2000;
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marker in a control non-overlan cancer manule. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker or anneals with a portion of the polynucleotide comprising the progression of ovarian cancer in a patient sample at a first point in time, repeating the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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marker in a patient sample and a normal level of expression of the
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21-DEC-1999; 99US-0171350P.
14-MAR-2000; 20000US-0189315P.
12-MAY-2000; 2000US-023031P.
09-JUN-2000; 2000US-0210600P.
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The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with

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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncardian cancer cells as compared to their expression in normal (i.e. noncarded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to calls of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer sample. A difference between the marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed marker is a portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein
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cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
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                                                                                                                     Sequence 500 BP; 145 A; 108 C; 99 G; 148 T; 0 U; 0 Other;
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                                                                                                                                                         1.4%; Score 24; DB 100.0%; Pred. No. 1; tive 0; Mismatches
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                                                                                                                                                                                                                                   1690 TAAGTACCTCGGCCGCGACCACGC 1713
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25-JUL-2000; 2000US-0220661P.
21-DEC-2000; 2000US-0257672P.
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                                                                                                                                                                                               Matches 24; Conservative
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15-JUN-2000;
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ADL42477/c
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fragment corresponding to the marker. The presence of protein or protein creament is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker or anneals with a portion of the polynucleotide comprising the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, colypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer of the invention. Note: The sequence data for this patent did not form part of the print of the pr
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ADL42086/C
1D ADL42086,
XX
AC ADL42086;
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DT 20-MAY-2004 (first entry)
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Human ovarian cancer DNA marker #;
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Human; ovarian cancer; ds; tumour
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Human; ovarian cancer; ds; tumour
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Homo sapiens.
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Homo sapiens.
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X 21-MAR-2001; 2001W0-US009126.
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X 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0211940P.
PR 25-MAY-2000; 200US-0211940P.
PR 25-MAY-2000; 2000US-0211940P.
PR 25-MAY-2000; 2000US-0210P.
PR 25-MAY-2000; 2000US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-0200US-020U
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corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the can marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker is a secreted protein or to a transcribed comparing the presence in the sample, a protein or protein creasponding to the marker. The presence of protein or protein creasponding to the marker. The presence of protein or protein creasponding to the marker. The presence of a transcribed comparing to the marker, under specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed comprising the marker, under stringent conditions. The polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions or patient which involves detecting expression of the marker in a patient camparing the level of expression for the marker in a patient camparing the level of expression converse in a patient camparing the level of expression converse in a patient camparing an ovarian tissue sample. A composition comprising a marker, the converse of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
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100.0%; Pred. No. 1;
ive 0; Mismatches 0; Indels
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25-JUL-2000;
21-DEC-2000;
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Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are

WPI; 2001-611502/70.

Lillie J;

Lee J,

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

21-DEC-2000; 2000US-0257672P

used to characterize stage, grade, histological type of ovarian cancer.

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The invention relates to inclear acts markers which are overspressed in cancerous) ovarian cells as compared to their expression in normal (i.e. noncarcant cancer cells as compared to their expression in normal (i.e. noncarcant) ovarian cells. The invention also relates to polypeptides cancerous) ovarian cells. The invention and selectively bind to the corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclectide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker the presence of protein or protein fragment or protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment is detecting the marker or anneals with a portion of the marker is also used for monitoring the presence of a transcribed comprising the marker in a patient corresponds of expression of the marker in a patient corresponding to the marker, under stringent conditions. The sample at a first point in time, repeating the marker in a patient corresponding to the marker, under stringent conditions the sample at a first point in time, repeating the marker in a subsequent condition or the marker in a protein or protein or expression of the marker in a practical or the marker in a practical or the marker in a practical or the mar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                     invention relates to nucleic acid markers which are overexpressed in
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                    Disclosure; SEQ ID NO 4993; 106pp; English.
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ADL41725 standard; DNA; 521 BP.
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07-JUL-2000;
25-JUL-2000;
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancercus) ovarian cells. The invention also relates to polypeptides cancercus) ovarian cancer introdicts that selectively bind to the cancercus) ovarian cancer introdicts that selectively bind to the perpending ovarian cancer involving inhibiting expression of a gene corresponding ovarian cancer involving inhibiting expression of a gene corresponding ovarian cancer involving inhibiting expression of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer supplementary to a marker of the invention. The marker in a patient sample and a normal level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer. The level of expression of a marker corresponds to a secreted protein or a transcribed corresponding to the more of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the marker, under stringent conditions. The marker is also used for monitoring the marker or anneals with a portion of the polymucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the marker or anneals with a subsequent time and comparing the level of expression of the marker in a patient conditions. The marker is also used for monitoring the marker or anneals with a subsequent time and comparing the level of expression of the marker in a patient which involves detecting expression of the marker in a patient time and comparing the level of expression of the marker is an educance represente a human ovarian cancer DNA marker of the controdice of the marker is an under of the prince of patien
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Homo sapiens FL/34633 gene, VIRTUAL TRANSCRIPT, partial sequence,
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I (Dages 1 to 1197)
Nieleen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., Mhite,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
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                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
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/tissue type="prostate"
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PPACGMASGSSQPWAAASAPPMLSSKASLCIPTRGPPPQPLWRTPAARSHWPIPHPCD
TACPAPLPVVLVAPRSTILSMSRTWTCRRWAVAPCRABKLMCSSSRS"
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Further information about the clone and the sequencing project available at http://mips.gsf.de/projects/cdna/. Location/Qualifiers
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                /gene="DKFZp686B17277"
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/organism="Homo sapiens"
/mol_type="mRNA"
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/dl_one="INAGE:5502726"
/tissue_type="retinoblastoma"
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/clone_lib="NHI MGC 67"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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BM460277.1 GI:18509317
EST.
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1 (bases 1 to 975)

1 (bases 1 to 975)

Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MG clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12141 row. f column: 07
High quality sequence stop: 659.
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCTGCCTGTCTACTGAGGACTCCACTGAG
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1197; Conservative 0; Mismatches
                                                                                                                                                                                                                                    1. .1197
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="t=xon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                     <1. .>1197
/gene="FLJ34633"
/locus_tag="HC11301"
                                                                                                                                                                                                             Location/Qualifiers
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(MGC)

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/tissue type="ductal carcinoma, cell line"
/lab host="milds" (phage-resistant)"
/clone_lib="NIH_MGC_110"
/clone_lib="NIH_MGC_110"
/clone_lorgan: paracreas; Vector: poTB7; Site_l: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the
following 5; adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Supersoript IIT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 ATGCCCGGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGA 103
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                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cagaba-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2390 row: o column: 22
High quality sequence stop: 535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC
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   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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917 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8341018 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249453
5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 917)
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CGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCTGCCCCT
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/cell_line="SNU-16"
/cell_line="SNU-16"
/lab_host="DHR0B"
/clone_lib="SSNU16n1"
/clone_lib="SSNU16n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_l: EcoRI;
Site_2: Not1; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."
                                                                                                                                                                                                                                BM823479 622 bp mRNA linear EST 06-MAR-2002
K-EST0094733 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-102-H01
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I (bases 1 to 622)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
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                                             934 CGCCCACAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCTGCCCCT 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAG 60
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
        814 ACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                874 GATGCTGAGGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consider Account of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Email: yongsung@mail.kribb.re.kr Plate: 102 row: H column: 01 High quality sequence stop: 622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.3%; Score 622; DB 3; Length 622; ilarity 100.0%; Pred. No. 3e-308; Conservative 0; Mismatches 0; Indels
                                                                                                         644 AGCCTGCCCAGCACTTTGCCAGTAGTCCTCGTGG 678
                                                                                      601 AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="$22$NU16n1-102-H01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'tissue_type="Ascites"
                                                                                                                                                                                                                                                                                              BM823479.1 GI:19179892
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                             , mRNA sequence.
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Homo sapiens (human)
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Matches 578; Conserv
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                                                                                                                                                                                           532
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                                                                                                                                                                                                                                                                                                                                        TGCGACACACACCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCCAGGAGTACTATT 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576 TTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGCCGCCTGG 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 TACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGG 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.

1 (bases 1 to 582)

2 (bases 1 to 582)

Mizuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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 'n
                                                                                                                                             CTGATCGTGCACCCCCCAGCCGGCGCATGGCCAGCGGCTCAACCATGGGCAGCA
                                                                                                                                                                                                             GCTTCAGCTACCCCGATGTTAAGGTCAAAGGCATCCCTGTGTATCCCTACCGAGGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                         GCTTCAGCTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCA
                                                                                                                                                                                                                                                       TGCGACACAGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATT
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                                                                                                                            CTGATCGTGCACCCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCA
                                                                                                Gaps
from DMSO-treated hES cell line H9 (p22) maintained feeder-free conditions"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                               7; Length 753
                                                                                           0; Indels
                                                             Query Match 34.9%; Score 59%; DB 7; Le Best Local Similarity 100.0%; Pred. No. 7.1e-296; Matches 59%; Conservative 0; Mismatches 0;
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BP315176.1 GI:52244151
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Contact: Yutaka Suzuki
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                                 DRIGIN
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AA316608 510 bp mRNA linear BST 19-APR-1997 EST188290 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          942 GACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGG 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGATCGATGAGCTGGCCAAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAA 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     882 GGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACA 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               822 GATCTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGGAGGATGCTGA 881
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                             1. .582
/organiam="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/clone="ORR07979"
/tissue_type="mammary gland"
/clone_lib="Sugano cDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 GACCTCGGAGGTCGTTCAACTCGGGCTGCTGCCCCCAACCGCTGCTGCCCCCTGAACGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCGAGCCGAGAAATTGATGTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462 CATGGGCAGCAGCTTCAGCTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTA
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1 (bases 1 to 510)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
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                                                                                                                                                                                                                                                                                                                                                                                         Length 582
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                                                                                                                                                                                                                                                                                                                                                                                         30.8%; Score 528; DB 3; I
99.8%; Pred. No. 7.9e-260;
iive 0; Mismatches 1;
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA316608.1 GI:1968936
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714

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p DNA linear GSS 02-JUN-2005
VIRTUAL TRANSCRIPT, partial
                                                         715 ATTGATGTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae, Pan.

I (Dases 1 to 1181)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,

Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,

White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

A Scan for Positively Selected Genes in the Genomes of Humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1181)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                 TTCCATGAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 GAGGAGTACTATTCTTTCCATGAGTCGGACCTGGCCCGGAGATGGGCAGTGGCTCC
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Pred. No. 9.6e-241;
0; Mismatches 1;
                                                                                                                                                                                                               /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xreff="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes FLJ34633 gene, VIR sequence, genomic survey sequence. D0045549 DQ045549.1 GI:66896764 GSS.
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/gene="FLJ34633"
/locus_tag="HC11301"
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99.8%;
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hamma, M.C., Hedblom, E., Hinkle, P. S.Jr., Kelley, J.M., Kelley, J.C., Liuli.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Philips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bedarik, D.P., Feng, D.F., Ferger, M.A., Colleman, T.A., Collins, E.J., Dimke, D., Kunsch, C., Hungjun, M.A., Gruber, J., Hustings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Oleen, H., Raymond, L., Wal, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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/cell_line="KM12C(HCC)metastasis into mouse (liver)"
/clone_lib="HCC cell line (matastasis to liver in mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="ATC" (inhost):113362"
/db_xref="taxon:9606"
/tissue_type="colon"
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The Institute for Genomic Research
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/organism="Homo sapiens"
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1 (bases 1 to 470)

2 (bases 1 to 470)

3 Bbert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

4 Human Unigeneset - RZPD3

4 Unpublished (2003)

5 Contact: Ina Rolfs

7 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

7 RZPD Deutsches Ressourcenzentsching No.972)

7 Human Unigeneset - RZPD3 (RZPDLIB No.972)

7 Human Unigenese Ressourcenzentsching fuer Genomforschung GmbH

7 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

7 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

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8 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

8 RZPD 149 30 32639 111
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470 bp mRNA linear EST 07-FEB-2003
BX110746 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGp998E036110 ;
IMAGE:2456810, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1397 TGGTCTGATCCCTGCCAGGGCCCCTTCCTTCCTGCTCATGGTCTTCAGGTGGCCTGATCA 1456
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This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
Ml3u, Primer sequence: CGTTGTAAAACGACGGCCAGT.
                                                                                                                                                         TGGGAGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCCTTGCCTTGGCTGG
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                                  Length 489;
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                          Query Match 28.0%; Score 480; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 4.1e-235;
Matches 480; Conservative 0; Mismatches 0;
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LiNL at:
Insert Length: 831 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 432.
Location/Qualifiers
                                                                                                                                                                                                                                                     GGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCC 1059
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                                                                                 CAGACCTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGT 999
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
AAGAICTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCT 879
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 489)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nlh.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                   GAGGCCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCA
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2456810"
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/clone='IMAGE:196020"
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/tissue type="choriocarcinoma"
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/lab_hote="Under type=resistant)"
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/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="organ: placenta; Vector: placenta; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 bp mRNA linear EST 17-SEP-2004
BP331524 Sugano cDNA library, rectum Homo sapiens cDNA clone
RCT09504, mRNA sequence.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM842 row: g column: 05
High quality sequence stop: 668.
Location/Qualifiers
1.966
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100.0%; Pred. No. 1.2e-219;
ive 0; Mismatches 0;
CDNA Library Arrayed by: The I.M.A.G.E.
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                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 450; Conservative
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/clone lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
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1 (bases 1 to 966)

11 (bases 1 to 966)

Nath-MOC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                       /mol_type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGD998B036110; IMAGE:2456810"
/tisuse_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 CTCCCTGGGGTAATTCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATTGGGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               26.3%; Score 450; DB 5; Length 470; 100.0%; Pred. No. 1.1e-219; ive 0; Mismatches 0; Indels
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                              organism="Homo sapiens"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE901537.1 GI:10390818
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Matches 370; Conserv
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             Hominidae; Homo.

1 (bases 1 to 583)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

Block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 bp mRNA linear EST 22-MAR-200
x827g07.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770908 3',
AWS89267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                      Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@img.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                             24.8%; Score 424; DB 3; Length 583; 100.0%; Pred. No. 2.9e-206; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                /tissue_type="rectum"
/clone_lib="Sugano cDNA library, rectum"
                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RCT09504"
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Homo sapiens
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Matches 424; Conservative
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CTCA 482
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Email: cgapbs-realilinib.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
image.lln!gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 361.
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13 bp mRNA linear EST 25-JUN-2003

EST19181 human nasopharynx Homo sapiens CDNA, mRNA sequence.

CD702656

CD702656.1 GI:32233286
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/mol type="max" septems
/db_xref="taxon:9606"
/dclone="lnAdB:2770908"
/tissue type="max" spooled tumors"
/db host="bhilds"
/db host="bhilds"
/clone lib="NCI GAAP Ut2"
/note="organ: ulerus; Vector: pCMV-SPORT6; Site_l: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
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Hominidae, Homo.
I (bases 1 to 370)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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                                                                                                                          Tumor Gene Index
Unpublished (1997)
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/tab host="http://www.near.com/lab host="http://www.near.com/lab host="near.com/lab host="bition" (GAP_Kid11" /clone_lib="NCI CGAP_Kid11" /note="forgan: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 1322376-1323911, 1456007-1456775, and 150052-1502855). Subtraction by Bento Soares and M. Parima Bonaldo.
                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Produrement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Produrement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CLone distribution: NG-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 236 Srd Error: 0.00

Seq primer: -40UP from Gibco.
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Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1436 GGTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 CCCTGACTCCATCCCCCTATTGCCACCTAACCAATCATGCAAACTTCTCCCTCGGG
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                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2296223"
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITCACTGGGCCATGGGATCTACATCTCCTTGCATCCCCAGCTGGTCTGATCCCTGCCAG 1414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1235 AAGCATGGCCTACAGAATGAAGAGGGGACCAGGAACCCCTGTGGGAGAGAGCTTAGACCT 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1295 GAAGCAGTGCCCACTCTGGCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCA 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 GGTACCCAGCAAGCCATGACTCATCCTTCCAGGCACCGACACAGACTCGTCGGGGGCAC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 CCTTGCTCCAGGTGTACTGCTAACCCCTGCCAGGCCCAGCTGCCACACCCTTTCTGGGAG 193
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 AAGCATGGCCTACAGAATGAAGAGGGGGACCAGGGAACCCCTGTGGGAGGGGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1115 GGTACCCAGCAAGCCATGACTCATCCTTCCAGGGCACCGACACAGACTCGTCGGGGGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .513 /-
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/clone_lib="human nasopharynx"
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library from southern Chinese"
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                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
( Dases 1 to 513)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G.
                                                                                                                                                                                                      Transcriptional Gene Expression Profile of Human Nasopharynx
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.9%; Score 323; DB 6; Length 513; 100.0%; Pred. No. 3e-154; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
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1 (bases 1 to 330)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                    Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
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                                                                                                                                                                                                                             Unpublished (2003)
Contact: YiXin Zeng
Cancer Center
                       sapiens (human)
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Best Local Similarity 100.
Matches 323; Conservative
                                                 sapiens
                         Homo
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nk07d10.81 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1012819 3',
                     mRNA sequence.
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/clone lib="NIH MGC 9"
/clone lib="NIH MGC 9"
/clone lib="NIH MGC 9"
/clone dito EcoRT/Xhol sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 ATGCAGCCCTGCCTGTCTACTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGC 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 CAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCGGGATGG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCCCTGTGTATCCCTACCCGAGGCCACCTCCCCAGCCCCTGATGCGGACTCCTGCTG 563
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                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov Plate: LLCM810 row: d column: 06
High quality sequence stop: 752.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 TGCCTTCTGCTTCCGCCGCTGCCGGATTGCCTCCAGCGCTGTGGAGCCTGTGTGGGGG
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1 (bases 1 to 1015)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
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Matches 403; Conservative
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ORGANISM
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EST 12-SEP-1997

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AA573775

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CDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 635 Std Brror: 0.00
Seq primer: -40ml3 Fwd. ET from Amersham
High quality sequence stop: 465.
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                             Hominidae; Homo.

1 (bases 1 to 556)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 556;
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Best Local Similarity 99.6%; Pred. No. 9.1e-138;
Matches 461; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1012819"
AA573775.1 GI:2348290
                                                 Homo sapiens (human)
Homo sapiens
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1538 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 ACTCTATGTTATGTTAAGGAGTTGGTTCTTGGCTGATGTTCTGTATCTTAACAT 35
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 TGGCTCCTCCTGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTCACTGGCCATGG
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Homo sapiens
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AW008047
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Matches 385; Conserv
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AW008047/c
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

Www-bio.llh.gov/bbrp/image/image.html
Seq primar: -40UP from Gibco
High quality sequence stop: 380.
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/clone_lib="NCI_carcinoid"
/clone_lib="NCI_carcinoid"
/clone_lib="NCI_carcinoid"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from meroendoorzine lung; vector lung darkinoid, and was then primed with a not Eco RI adaptors (Pharmacia), digested with Not I and to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                 AI216202 412 bp mRNA linear EST 22-OCT-1998
qm37e07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1884036 3',
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274 TCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACC 215
                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 412)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                             1560 TICAACAGITAAAAGAAGCITAICITAAAIGTAITGIATIGGG 1602
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/note="Organ: Stomach; Vector: The decapped with bacterial alkaham and purchash and stomach; Vector was educated to have about Gont. The CDNA westor was adjusted to have about Gont. The CDNA westor was adjusted to have about Gont. The CDNA westor was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM750392 246 bp mRNA linear EST 04-MAR-2002
K-EST0025949 S7SNU719 Homo sapiens cDNA clone S7SNU719-1-G12 5',
mRNA sequence.
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1 (bases 1 to 246)

1 (bases 1 to 246)

1 (bases 2 to 246)

2 (bases 3 to 246)

3 (bases 3 to 246)

4 (bases 3 to 246)

5 (bases 4 to 246)

6 (bases 4 to 246)

6 (bases 5 to 246)

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7 (bases 7 to 246)

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9 (bases 7 to 246)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are
                                                                                                                                                                      CAGCCCTGCCTGTCTACTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 148
                                                                                                                                                                                                                                                                                  327 CAGCCCCTGCCTGTCTACTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 386
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                         CTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCGCTGTGGAGCCTGTGTGCGGGGGATG
                                                                                                                                                                                                                                                   GGAGCACAATGGAGTGCCCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCGGGATGGCCA
                               CTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCGCTGTGGAGCCTGTGTGCGGGGATG
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Eax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: G column: 12
High quality sequence stop: 246.
                                                                                                                                                                                                                                                                                                                                                          447 GCGGCTCAAGTCAACCATGGGCAGCAGCTTCAG 479
                                                                                                                                                                                                                                                                                                                                                                                            GCGCTCAAGTCAACCATGGCAGCAGCTTCAG 241
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Unpublished (2002)
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/organism="Homo sapiens"
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BM750392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bы162756 21-JUN-2000 PM1-HT0454-170100-003-£07 HT0454 Homo sapiens CDNA, mRNA sequence.
BE162756.
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1 (bases 1 to 244)

Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., de Silva, W. F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
CAGGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTAT 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PMI-HT0454-170 100-003-f07&t3=2000-01-17&t4=1)
Seq primer: puc 18 forward
                                                                                                                                         CAGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTAT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                               CCTGGGGTAATTCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATTGGGGGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                CTTAACATGACCACAGTTTGTAAGTAC 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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Location/Qualifiers
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Matches 213; Conservative
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REFERENCE AUTHORS

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1...1092
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/clone="IMAGE:3629848"
/tissue type="choriocarcinoma"
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/clone lib="MNH MGC_21"
/clone lib="NHH MGC_21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1637 AGTTGGTTCTGGCTGATGTTCTGTATCTTAACATGACCACAGTTTGTAAGTAC 1696
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In (bases 1 to 1092)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

In oppublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/Linu at: image.llnl.gov

Plate: LLCM317 row: a column: 17

High quality sequence start: 19

High quality sequence start: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GCTTATCTTAAATGTATTGTATTGGGGGGGGGGCGCCCACTCTATGTTATGTTAAGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                      Score 180; DB 2; I
Pred. No. 1.3e-80;
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.00.0%; Pred. No. 3.3e-68;
                                                                                                                                                 10.5%; Sco...
100.0%; Pred. No. ...
... 0; Mismatches
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BE409561
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/note_2: Sma1; A mini-library was made by cloning products
Site_2: Sma1 A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
no 196,716 - Ludwig Institute for Cancer Research)
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                                                                                                                                                                                                                                                                                                                                                                                 1549 CCCTGGGGTAATTCAACAGTTAAAAGGCTTATCTTAAATGTATTGTATTGGGGGGGTGG 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1609 GCAGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTA 1668
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Fax: +55-11-2707001
Email: ssimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-HT1265-17401-002-0407&t3=2001-04-17&t4=1)
Seq primer: puc l8 forward
High quality sequence start: 10
High quality sequence stop: 284.
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MR4-HT1265-170401-002-d07 HT1265 Homo sapiens CDNA, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \operatorname{Simpson}, A \cdot J \cdot Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                             1489 GAGTGAACCCTGACTCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCT
                                                                                                                                                                                                                                                                                                             28 GAGTGAACCCTGATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCT
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10737800
                                                                                                      Length 246;
                                                                                                                                                                          Indels
   full-length enriched cDNA library."
                                                                                                   12.1%; Score 208; DB 3; I
100.0%; Pred. No. 4.7e-95;
iive 0; Mismatches 0;
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                                                                                                                                          Best Local Similarity Lou. Matches 208; Conservative
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                                                                                                              Query Match
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BG998476
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/mol_type="mRNA"
/db xref="laxon:9666"
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/clone="lange:196898"
/tissue type="choriocarcinoma"
/clone lib="NIH MGC_21"
/note="organ: placenta; Vector: pOTB7; Site 1: XhoI;
/note="organ: placenta; Vector: poTB7; 
                                                                                                                                                          AW732798 11-APR-2000
bb14f07.yl NIH_MGC_21 Homo sapiens cDNa clone IMAGE:2962885 5',
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RCO-FW0204-221200-022-b01 FN0204 Homo sapiens CDNA, mRNA sequence.
BF856421. GI:12244165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/irseources.shtml
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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8.1%; Score 139; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 139; Conservative 0; Mismatches 0; Indels
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/organism="Homo sapiens"
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Seg primer: -40RP from Gibco
High quality sequence stop: 112.
205 TGCCGGGCTGCTTCTGCTTCCGCC 229
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 139)
                                                                                                                                                                                                                            mRNA sequence.
AW732798
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TITLE
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                                                                                            RESULT 26
AW732798
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BF856421
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE741110 623 bp mRNA linear EST 15-SEP-2000 601593919F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947885 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="addinocarcinoma cell line"
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/lab host="DHIOB (phage-resistant)"
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                              GTGGGAGCGCCAACAGAGCTATGTCTGGAGACATATGATAAAACCACCTCAGCCCCCACC
                                                                                                                                                              218 AAGCCGCCGCACCCGTAGACCCGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCAT 277
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW810 row: e column: 06
High quality sequence stop: 615.
Location/Qualifiers
                                                                                                                               AAGCCGCCCCCCACCCACACCCCAAAGGACCCTGGCCACCATGGGCCAGAGAGCAT
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1 (bases 1 to 623)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:3947885"
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DKFZP469G0138 r1 469 (synonym: pkidl) Pongo pygmaeus cDNA clone DKFZp469G0138 5', mRNA sequence.
                                                                                                          1 (bases 1 to 277)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                                                                                                                                                                                                                                               Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 101; DB 3; Length 277;
100.0%; Pred. No. 6.1e-40;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                     Kim, Y.S.
21C Frontier Korean EST Project 2001
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                                                                                                                                                                                                                                                                                                                                                                                             Email: yongsung@mail.kribb.re.kr
Plate: 20 row: C column: 05
High quality sequence stop: 277.
Location/Qualifiers
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CR763815.1 GI:52602277
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sapiens (human)
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Contact: Kim YS
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BQ081980 GI:19938986
EST.
                                                                                                                   Hominidae; Homo.

1 (bases I to 450)

1 (bases I to 450)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunsteain,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2=RCO-FN0204-221200-022-b01&t3=2000-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 72
High quality sequence start: 72
High quality sequence stop: 446.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: prostate_normal; Vector: puc18; Site_1: Snal; Site_2: Snal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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316 CTTCTCCCTCCCTGGGGTAATTCAACAGTTAAAAGAAGGT 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                     Homo sapiens
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This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKF2);
Emall s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG315647 1014_MGC_21 Homo sapiens cDNA clone IMAGE:4541898 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="469 (synonym: pkid1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 GAGCGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GAGCGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCCACCAAGC 179
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.
1 (bases 1 to 276)
Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                        Pongo pygmaeus mRNA (Ansorge,W., Krieger,S., Regiert,T., et al.)
Unpublished (2004)
Contact: MIPS
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
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/mol_type="mRNA"
/db xref="mRNA"
/db xref="mRNA"
/lobme="IMAGE:4541898"
/lab host="Dillab"
/lab host="Dillab
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1.7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-50-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-062016.F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 CGCCCAACAGAGCTATGTCTGGAGACATATGATAAAC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CGCCCAACAGAGCTATGTCTGGAGACATATGATAAAC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Le
7.9e-38;
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 7.9
Matches 97; Conservative 0; Mismatches
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http://image.llnl.gov
Plate: LLCM1221 row: c column: 19
High quality sequence stop: 496.
Location/Qualifiers

    .928
    /organism="Homo sapiens"

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AG071655.1 GI:16623457
GSS.
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AG071655
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SOURCE
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LOCUS
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SOURCE
                                                                          RESULT 33
                                                                                              BG335025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Famil: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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                                                                                                                                                                                                                               1244 CTACAGAATGAAGAGGGGACCAGGAACCCCTGTGGGAGGGCCTTAGACCTGAAGCAGTG 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                       Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Obackenbush, J. and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clome_lib="MARC 2PIG"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
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0
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0
                                                        /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                  5.0%; Score 86; DB 10; Length 677;
100.0%; Pred. No. 3.6e-32;
tive 0; Mismatches 0; Indels
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239074 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF191474
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3.4%; Score 59; DB 2; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 59; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
USDB, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                           1304 CCCACTCTGGCTCCTCCTGCCTTGGC 1329
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/mol type="maxna"
/db_xref="taxon:9823"
/tissus_type="pooled"
/lab_host="DH10B"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-062016.F"
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Plate: 66 row: F column: 19
Seg primer: ATTTAGGTGACATARG.
Location/Qualifiers
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PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                          86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (pig)
                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                      Query Match
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ORGANISM
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COMMENT
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BF191474
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790 TCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCAC 848

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/clone='InAGE:4541320"
/tissue_type="choriocarcinoma"
/tissue_type="choriocarcinoma"
/tab.note="Dobe="Unit Bolidae-resistant)"
/clone lib="NHH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="organ: placenta; Vector: poTB7; Site_1: Vector: placenta; Ve
                                                                                                                                                                                                                                                                                                      BG335025 1088 bp mRNA linear EST 27-FEB-2001
602403470F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541320 5',
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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I (bases 1 to 1088)

S NIH-Mac http://mac.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Genomics, Inc.

CLONE Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://imagge.llnl.gov

Plate: LLCM1219 row: k column: 17

High quality sequence stop: 556.
266 TCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 CACCATGGGCCAGAGAGCATTACCTTCATCTTCTGGCTCTGAGCCGGCCCTTGAGT 342
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/db_xref="taxon:9606"
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BG335025.1 GI:13141463
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Sus scrofa
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tes 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                        Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
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1009 bp mRNA linear EST 16-DEC-200
8707606 RIKEN full-length enriched, 10 day old male pancreas Mus
musculus cDNA clone 1810019J16 5', mRNA sequence.
BY707606
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                               Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly Mann (2002)
12226715
Pahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
Quackenbush,J. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="MARC 2PIG"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
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                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4369 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 30 row: H column: 14
Seg primer: ATTTAGGTGACATATAGG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                      Contact: Smith TPL
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AUTHORS
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KEYWORDS
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                                                                                     TITLE
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Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper sealected cDNAs to prepare full-length cDNA libraries for trapper sealected cDNAs to prepare Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teagdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Watenabe, Y., Watenabe, Y., Watenabe, Y., Wang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itoh, M., Kagawa, I., Miyazaki, A., Hashizume, W., Imotani, K., Ishii, Y., Shinay, A., Yashino, R., Sakai, K., Sasaki, D., Shibata, K., Shinayawa, A., Yashunishi, A., Yashino, M., Waterston, R., Lander, B.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fel: 81-45-503-9212
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J. Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Horit,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
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/clone_lib="RIKEN full-length enriched, 10 day old male
pancreas"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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100.0%; Pred. No. 6e-08;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 420, 563-573 (2002)
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ACCESSION

VERSION KEYWORDS

BX518790 LOCUS

AUTHORS

REFERENCE

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EST 09-MAR-1998
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                1 (bases 1 to 406)
Marram., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousest@watson.wustl.edu
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut.
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA856355 491 bp mRNA linear EST
vw99g12.r1 Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:1263142 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="embryo"
/dev_stage="13.5-14.5dpc_total_fetus"
/lab_host="DH10B"
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1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.2%; Score 38; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: mob.REGA+ET
High quality sequence stop: 358.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:372517"
                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA856355
AA856355.1 GI:2944657
                                                                                                                                                                                                                                                                                             Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .406
                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:233949
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CEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W61708 406 bp mRNA linear EST 07-JUN-1996 md57£07.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:372517 5', mRNA sequence.
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                       EST 27-JUN-2003
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                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutherla, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Musinae, Mus.
1 (bases 1 to 378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free from RZPD; conteat RZPD; Choneerzpd.de) for further information. Seg primer: T7, Primer sequence: TAATAGGACTCACTATAGGG. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RZPD; IMACGOSGEL23179.

RZPDLIB; IM.A.G.E. cDNA Clone Collection;

ROBE Unigeneset - RZPDZ (RZPDLIB No.981)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response71ibNo-981 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Fax: +49 30 32639 111

www.rzpd.de
                                                                                                                                                                                                                                                                                                                                    Mouse Unigeneset - RZPD2
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                  BX518790 area thymus 2NbMT Mus musculus cDNA clone IMAGP998L233179 ; IMAGE:1263142, mRNA sequence.
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100.0%; Pred. No. 1.8e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGp998L233179 ; IMAGE:1263142"
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/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Thymus"
/dev_stage="4_weeks"
/lab_host="DH108"
                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
                                                                                                             BX518790.1 GI:32300318
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W61708.1 GI:1368457
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Best Local Similarity
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W61708
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PEATURES

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Gaps

Matches

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ORIGIN

AUTHORS

FEATURES

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This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@inage.lln.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 501)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
           Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="embryo"
/dev_atage="115-14.5dpc total fetus"
/dab_host="billoB"
/clone_lib="Soares mouse embryo NDME13.5_14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZOS9937
RPCI-23-429E10.TV RPCI-23 Mus musculus genomic clone RPCI-23-429E10, genomic survey sequence.
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Local Similarity 100.0%; Pred. No. 1.8e-07;
tes 38; Conservative 0; Mismatches 0;
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                  1. .500
/organism="Mus musculus"
                                                                                                                            Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                   quality sequence stop: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:372517"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                               Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6J"
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="unknown"
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AZ059937.1 GI:7351186
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                                                                                                                                                                                                                                       correct orientation)
  Unpublished (1999)
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POLYA=No.
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Ten, F., Underwood, K., Morre, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Ritter, E., Kohn, S., Shin, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:665694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                          The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyNouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
Email: mouseest@watson.wustl.edu
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -28ml3 rev2 ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:10090"
/clone="IMAGE:1263142"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
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GSS 30-MAR-2000

RESULT 39

ORIGIN

AI425628

KEYWORDS

REFERENCE AUTHORS

TITLE

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Contact: Kachar, B.
Structural Cell Biology
    Seg primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.C
Matches 38; Conservative
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Kachar, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (RRL Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE652359
UI-M-AOO-aca-d-03-0-UI.rl NIH BMAP MPG Mus musculus cDNA clone
UI-M-AOO-aca-d-03-0-UI 5', mRNA sequence.
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CHOM Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
                                                                     Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgaen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
1 (bases 1 to 519)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Mational Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-8643, USA
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9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2%; Score 38; DB 9; Le
ilarity 100.0%; Pred. No. 1.8e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="RPCI-23-429E10"
                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Female"
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Fax: 301 443 9890
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Matches 38; Conserval
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DEFINITION
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AUTHORS
TITLE
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COMMENT
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/ Burathe - 2.0.00 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0 / 2.0
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/dev stage="Post natal day 5 to 13"
/dev stage="Post natal day 5 to 13"
/clone lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
C as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P0;
14 from P12 and 24 from P13. After killing animals by
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Mammalia, Eutheria, Euarchontogilres, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
(bases 1 to 535)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligo-dT track. The library was constructed as descril
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996. Tissue provided by Ms. Annie Novakovich,
Zivic-Miller Laboratories."
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Plate: 52 row: a column: 07
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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                                                                                                            /organism="Mus musculus"
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/clone="gi52a07"
Location/Qualifiers
                                                                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6J"
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Mus musculus
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/strain="BALB/c"
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REFERENCE

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cervical dislocation followed by decapitation, the bullar was removed and opened in Leibowitz medium. The bony cappule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fastrack kit (catalog # K1592-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector Kit (catalog # 237211, Stratagene) and Uni-Zap XR digapack III Gold Cloning kit (catalog # 237612), both from Stratagene [La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Fth DNA polymerase and RNase H. Complementary DNA was blunt ended with Fth DNA polymerase, ligated with ECON I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over pharmacia Size Seps00 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Altro, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with ECON Lecombinants Stratagene's Exassist Interference resistence helper phage (catalogue # 211203) was adopted resistence believe pharmacia continue with the content of from 20 ul of saturated culture with the content of from 20 ul of saturated culture with the content of from 20 ul of saturated culture with the content of from 20 ul of saturated culture with the content of from 20 ul of saturated culture with the submaint server and since penetated with the submaint server prime of the phage primer (CAGAGAGCTARACACCTARACACCTARACACCTARACACCTARACACCTARACACCTARACACCTARACACC
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586 bp mRNA linear EST 18-DEC-2003
H308EC02-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
BG082830
                                                                                                                                                                                                                                                                                                     Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                         Gaps
   2.2%; Score 38; DB 5; Length 535; 100.0%; Pred. No. 1.8e-07; tive 0; Mismatches 0; Indels
                                                                                            340 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 377
                                                                          835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 872
                                                                                                                                                                                                                                                                     BG082830.2 GI:40069253
Query Match
Best Local Similarity 100.0
Matches 38; Conservative
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KEYWORDS
SOURCE
                                                                                                                                                                               BG082830
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BB657667 BB657667.1 GI:16491493

ACCESSION

VERSION

The state of the s

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/done libe WIA Mouse 15K CDNA Clone Set"
/done libe WIA Mouse 15K CDNA Clone Set"
/dote="Vector: pSPORT1; Site 1: Sal1; Site 2: Not1; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastcoyst, embryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary CDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo (dT).Not primars. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse development CDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale CDNA analysis reveals phased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bmail: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3081 row: C column: 02
Seg primer: -21M13 Reverse
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BB657667 RIKEN full-length enriched, 12 days embryo eyeball Mus musculus cDNA clone D230011M17 5', mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.
Sciurognathi; Muroidea; Murinae; Mus.
I (basea 1 to 586)
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                On Jan 26, 2001 this sequence version replaced gi:12565398.
Other_ESTs: H3081C02-3
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1.9e-07;
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/db_xref="taxon:10090"
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/mol_type="mRNA"
/strain="C57BL/6J"
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COMMENT

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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Birect Submission

L Submitted (17-NOY-2003) Masahira Hattori, The Institute of Physical

Submitted (17-NOY-2003) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokoham, Kanagawa, 230-0045, Japan

(B-mail: hattoriegsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC

library availability, please contect Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute, Bio Resource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199
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                                                                                                                                                                                                                                                                                                                                                                                                                         AG603040 763 bp DNA linear GSS 23-DEC-2004
Mus musculus molossinus DNA, clone:MSMg01-535K05.T7, genomic survey
was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
Shiroishi,T.
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1.9e-07;
hes 0; Indels
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/tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                           2.2%; Score 38; DB 2; Length 601;
100.0%; Pred. No. 1.9e-07;
ative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9
:ive 0; Mismatches
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/sub_species="molossinus"
/db_xref="taxon:57486"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG603040
AG603040.1 GI:48363870
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Best Local Similarity 100.09
                                                                                                              Query Match 2.23
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Matches 38; Conservative
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AG603040/c
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Pukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs, Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-rese@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                  1 (bages 1 to 601)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J.,
Komno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Takeda, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                       Euteleostomi;
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/dev_stage="12 days_embryo"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="D230011M17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
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                             Mus musculus (house mouse)
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                          SOURCE
ORGANISM
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JOURNAL
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                                                                                                                                                                                                  AUTHORS
  CEYWORDS
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/mol_type="mRNA"
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BI413848
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918 bp mRNA linear EST 24-OCT-2000 e0177134F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014680 5',
                                                                                                                           BI694617
601347838F1 NCI_CGAP_Mam2 Mus musculus CDNA clone IMAGE:5375384 5',
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rømail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.llnl.gov

Plate: LLAM11955 row: 1 column: 09

High quality sequence stop: 796.
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//note="Organ: mammary; Vector: pCWV-SPORT6; Site 1: SalI;
Site_2: NotI; Cloned unidiractionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Mus.
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/.
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462 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="INMGE:5375384"
/tissue_type="tumor, biopsy sample"
/dev stage="5 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2%; Score 38; DB 3; Le
Local Similarity 100.0%; Pred. No. 1.9e-07;
Ne 38; Conservative 0; Mismatches 0;
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/strain="FVB/N-3"
                                                                                                                                                                                                                                              Mus musculus (house mouse)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Parayed By: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 653.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/#strain="Czech II"
/db_txref="tzaxon:10090"
/clone="type="tumor, metastatic to mammary"
/lab hoft="MluB"
/clone lib="NOI CGAP Lu30"
/clone lib="NOI CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by WMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayd by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Phttp://mage.llnl.gov
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602991514F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5147642 5',
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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100.0%; Pred. No. 1.9e-07;
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Matches 38; Conservative 0; Mismatches
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/organism="Mus musculus"
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High quality sequence stop: 840.
Location/Qualifiers
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Mus musculus
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100.0%; Pred. No. 2e-07; iive 0; Mismatches 0;
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AK051860
AK051860.1 GI:26342255
                38; Conservative
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 Local Similarity
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S NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Nammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: capaba-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
           /clone lib="NCI_CGAP_Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sal1; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                              Length 930;
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Local Similarity 100.0%; Pred. No. 1.9
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High quality sequence stop: 629.
Location/Qualifiers
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/clone="IMAGE:4008914"
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/strain="Czech II"
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2.2%; Score 38; DB 2; Length 984;

Query Match

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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramateu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 1596)
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
enriched library, clone:D230011M17 product:hypothetical protein,
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
         Gaps
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Indels
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Hiraoka, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kasukawa, T., Kato, H., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Saakai, T., Sagabe, Y., Shinata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Yoshida, K., Yoshina, M., Muranatsu, M. and Hayashizaki, Y., Tohida, K., Yoshina, M., Muranatsu, M. and Hayashizaki, Y. Direct Submission
Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, MRINEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, URI:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_grage="10 day old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:1810019J16"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/bstrain="CS7BL/6J"
/db_xref="FANTOM_DB9.D230011M17"
/db_xref="taxon:10090"
/clone="D230011M17"
/tissue type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="l2 days embryo"
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GLQPRTQAPQRCRQSLQRRKQXAALHQSQPQGRQRRQQVGGSLAGSAEPEMKVILSGP
WWPGSLGSGLLVRRPGGGWERSSFVSRHNSDGLSQGPKRGGPDDGRGCPGLGMAQSMA
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                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810019316 product:SIMILAR TO TATA BOX BINDING PROTEIN (TPB) -ASSOCIATED FACTOR, RNA POLYMERASE II, C1, 130KD homolog [Mus musculus], full insert sequence.
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(evidence: decoder, Longest-ORF)
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Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Managawa 230-0045, Japan (B-mail:genome-resegue.riken.jp, URL:http://genome.gec.riken.jp, 761:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
1..1596
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High-efficiency full-length cDNA cloning
Math. Enzymol. 303, 19-44 (1999)
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/db_xref="G1:26342256"
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Couract: Gozen istylmore National Research of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-31 Talabido, Setagaya, Tokyo 154-8567, Japan
Tel: 81-3-3149-2476
Fax: 81-3-3149-2476
Fax: 81-3-3149-2252
Email: gtsylimotcomch.go.jp
This work was performed to collaborate with Developmental Biology
Department, National Institute of Agrobiological Sciences. Address:
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
81-29-838-8633 e-mail: kazuha@affrc.go.jp
This work was funded by Organized Research Combination System
(ORCS) project of Ministry of Education, Culture, Sports, Science
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H.,
Suzuki, Y., Tsujimoto, G., Izaike, Y., Todoroki, J. and Hashizume, K.
Characterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray
Mol. Reprod. Dev. 65 (1), 9-18 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                             BP111348 SRCS bovine utero-placenta cDNA Bos taurus cDNA clone
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.
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/dev_stage="adult"
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2.2%; Score 37; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 37; Conservative 0; Mismatches 0;
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1 (bases 1 to 605)
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Location/Qualifiers
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Contact: Gozoh Tsujimoto
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hes 35; Conserv
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                                                             DRIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lumblished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Tissue Procurement: M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
Nww-bio.llnl.gov/bbrp/image/image.html
Insert Length: 792 Std Error: 0.00
Seq primer: -40UP from Gibco.
High quality sequence stop: 452.
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/note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker: Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and se
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
                                                                                                                                                                                                                         ASSGAPCYGTGYGLPSASDAAGIACSAVĞLVCGAAAPALSAGDPIEGSAEAAWAKEHN
GVPPSPDRAPPSRRDGQRLKTSMGSSFSYPDYKLKGTPYYPYHATSBYPDVDSCCKB
PLABEPPPTRHSLPSTFTNSPRGSEBYYSFHESDLDLPEMGSGSMSSREIDVLIFKKLT
BLFSRYQIDELAKCTSDYPEKTSKISDLISSITQDYHLDEQDAEGRLVRGIIRIST
RKSRSRRQTDELAKCTSPPYPAAPDSGHBTMLGSGLSQDBLIYQISGEFTAADAIRIST
RKSRSRRAGTABARAGTAPAAAPDSGHBTMLGSGLSQDBLIYQISGEFTAADAIRKL
RPYGAPGYPASQDSSFQGTDTDSSGAPLLQVYC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI669760 488 bp mRNA linear EST 15-DEC-1999 1112h08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2250879 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                    /translation="MSAPSPHRAVAPGGOTLRTLATTGORVSPSFOALONOPTSPOPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, C1, 130KD homolog [Mus musculus] (SPTR|Q922Q0, evidence: FASTY, 97.2%ID, 100%length, match=649)
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1 (bases 1 to 488)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 2.2%; Score 38; DB 4; Length 1657; 1 Similarity 100.0%; Pred. No. 2.1e-07; 38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       882 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          835 ATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCA 872
                                                                                                                                         /proteIn_id="BAC25177.1"
/db_xref="GI:26357449"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2250879"
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/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                        putative"
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A1669760/c
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Gaps

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Gaps

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CB759331 434 bp mRNA linear EST 16-MAY-2003 AMGNNUC:NRP14-00055-F9-A W Rat pituitary (10472) Rattus norvegicus cDNA clone nrpi4-00055-F9 5', mRNA sequence.
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601235445F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3599314 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:10116"
/clone="mrnyi4-00055-f9"
/clone="mrnyi4-00055-f9"
/clone="mrnyi4-00055-f9"
/clone="my rat pituitary (10472)"
/note="vector: pSPORTI; Site I: Sall; Site 2: Not1; W Rat pituitary adult female Wistar rat avg insert size 2: Lkb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus
                                                                                                                                                              /cell type="Embryonic Stem Cell"
/clone lib="Sanger Institute Gene Trap Library pGT2lxr"
/note="Vector: pGT2lxr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Plate: 00055 row: f column: 9.
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                                                                                                                                                                                                                                                                                 1.7%; Score 29; DB 10; Length 260; 100.0%; Pred. No. 0.0074; Pred. No. 0. 100618
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5. 0.0078; 0; Indels
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    .434
    /organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                                                                                                                        208 TTCAAGAAGCTGACAGAGCTGTTCAGCGT 180
                                                                                                                                                                                                                                                                                                                                                                                  730 TTCAAGAAGCTGACAGAGCTGTTCAGCGT 758
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                                                   organism="Mus musculus"
                                                                    /mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
       Location/Qualifiers
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Amgen RST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Pitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
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EST.
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BE533148
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Matches 29; Conserv
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AUTHORS
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BE533148
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

1 (bases 1 to 260)

13 (bases 1 to 260)

14 (bases 1 to 260)

15 (bases 1 to 260)

16 (bupublished (2003)

17 (bupublished (2003)

18 (contact: Sanger Institute Gene Trap Resource - SIGTR

Wellcome Trust Sanger Institute Gene Trap Resource - SIGTR

Wellcome Trust Sanger Institute

Email: info.penetrappsanger.ac.uk

Sequence tag generated by 5, RACs of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from Sanger Institute Gene Trap

Resource. Annotation information available from

http://www.sanger.ac.uk/PostGenomics/genetrap/

Class: Gene Trap.
                                                                                                                                                                                                                                                                                             USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Email: smitth@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: LAM8004 row: M column: 8
Seq primer: GTAATACGACTACACTATAGGG.
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Peccora; Bovidae; Bovinae; Bos.

1 (bases 1 to 585)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Contact: Smith TPL
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/note="Vector: pcDNA3.1; Site 1: BcoR1; Site 2: Not1;
Library made with RNA pooled from multiple tIssues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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BC0173 Sanger Institute Gene Trap Library pGT21xr Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH108"
  GI:29269819
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                                                   Bos taurus (cow)
    CB463434.1
                                                                      Bos taurus
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1.7%; Scor.
100.0%; Pred. No. v...
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100.0%; Pred. No. 0.0
iive 0; Mismatches
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                            organism="Mus musculus"
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  ocation/Qualifiers
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                                                                                     strain="FVB/N-3"
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BG871324
BG871324.1 GI:14221864
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Matches 29, Conservative
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Matches 29; Conservative
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                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabe=remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Presyed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
ticolumn: 11
High quality sequence stop: 587.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="Dillo"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Öligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrasque by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.m.column: 03
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                1 (bases 1 to 609)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                    Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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100.0%; Pred. No. 0.008;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:3599314"
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/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: Sali, Cloned unidirectionally. Primer: Olīgo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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/db xref="taxon:10090"
/clone="IMAGE:5005226"
/tissue type="tumor, biopsy sample"
/dev_stage="5 months"
/lab host="0H108"
/lab host="Organ: mammary; vector: pCMV-SPORT6; Site 1: Sall;
Site_2: NOLI; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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1 (Dases 1 to 756)
NIH-MGC http://mgc.nci.nih.gov/.
Nith-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Tree E. Cornologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMLOGY row: c column: 22
High quality sequence start: 114
High quality sequence stop: 750.
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/clone="IMAGE:4923597"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_SG2"
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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

BF041373

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ACCESSION

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AL730744 629 bp mRNA linear EST 18-APR-2002 AL730744 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA clone BNOAA116ZH12 5', mRNA sequence.
                                                                                                                                                                Danio rerio

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleosted; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

Colmbra, K. Weil, D., Brottier, P., Blanchard, S., Levi, M.,
A subtracted CNRA library from the zebrafish (Danio rerio)
embryonic inner ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
AL724130 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BNOAA0732B04 5', mRNA sequence.
AL724130
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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100.0%; Pred. No. 0.026;
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live 0; Mismatches
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/dev_stage="embryonic"
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/organism="Danio rerio"
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/organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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                                                                                                 AL724130.1 GI:20188734
                                                                                                                                               Danio rerio (zebrafish)
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Contact: Genoscope
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AL730744/c
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Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
tto H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                              BF041373 485 bp mRNA linear EST 10-OCT-2000 BP250025B20B12 Soares normalized bovine placenta Bos taurus cDNA clone BP250025B20B12 5', mRNA sequence.
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1 (bases 1 to 485)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Lewin, H. A.
W. McKeck Center for Comparative and Functional Genomics
W. Dilinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lob host="DH108"
/clone_lib="Soares normalized bovine placenta"
/clone_lib="Soares normalized bovine placenta"
/note="Organ: placenta; Vector: pT773Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806."
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100.0%; Pred. No. 0.026;
tive 0; Mismatches 0; Indels
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BACKWARD: ATTAACCTCACTAAAG
Insert Length: 485 Std Brror: 0.00
Plate: BP250025B20 row: B column: 12
Seg primer: AGCGATAACATTTCACACAGGA
High quality sequence stop: 485.
Location/Qualifiers
                                                                        216 AAGGACCCTGGCCATGGGCCAGAGAG 244
                                                142 AAGGACCCTGGCCACCATGGGCCAGAGAG 170
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/clone="BP250025B20B12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Conservative
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Fax: 217 244 5617
                                                                                                                                                                                                                                                                                                                                                         Bos taurus (cow)
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FEATURES

RESULT 61 AL724130/c LOCUS

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AI267255 Stanley Frontal SN pool 2 Homo Bapiens CDNA clone IMAGE22035545, mRNA sequence.
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.

Dubort Wheat cDN2 Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2602
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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I (bases 1 to 535)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Washu-NCI human EST Project

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@inage.llnl.gov) for further information.
Seq primer: -40UP from gibco
High quality, sequence stop: 442.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               /clone="wpils.pk007.a7"
/tissue type="leaf"
/tissue type="leaf"
/clone_lib="wpils"
/note="Vector: PGEM-T Basy; Site 1: Smal; Wheat, Polk
cultivar (resistant), infected with septoria tritici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .535
/organiam="Homo sapiens"
/organiamsnha"
/db_xref="t-axon:9606"
/clone="IMAGE:2035545"
/lasue_type="frontal lobe (see description)"
/lab_host="DH10B" (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6%; Score 27; DB 6; Length 369;
100.0%; Pred. No. 0.082;
trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             /organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
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AI267255.1 GI:3886422
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Best Local Similarity
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AI267255/c
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1 (bases 1 to 369)
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( bases I to 765)

Coimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:7955"
/clone="BNOAAA011ZE08"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
              /clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                    inner ear subtracted cDNA Danio
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
_Location/Qualifiers
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                                                                                                                             Length 629;
                                                                                                                        Query Match 1.6%; Score 28; DB 1; Length 629
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 28; Conservative 0; Mismatches 0; Indels
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rerio CDNA clone BNOAA0112E08 3', mRNA sequence.
AL715958
                                                        /note="subtracted cDNA library"
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Triticum aestivum
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Unpublished (2002)
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CA736276
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Query Match 1.6%; Score 27; DB 6; Length 600; Best Local Similarity 100.0%; Pred. No. 0.086; Matches 27; Conservative 0; Mismatches 0; Indel8
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Danio rerio
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Unpublished (2002)
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/clone_lib="Stanley Frontal SN pool 2"
/note="Organ: brain; Vector: pGR2.1-rOPO (Invitrogen);
Site_1: EcoR1; Total RNA (purified with Trizol and DNAsed
before use) was reverse transcribed using a modified
oligo-dT primer containing Real and HindIII sites.
Oligo-dT primer containing Real and HindIII sites.
Double- stranded cDNA was digested with Real, resulting in
blunt ended cDNA was gplit into two sets, one used as is as
the driver, the other set was split in half again and each
half linked to a different adaptor.
S'-TCGAGCGCCCCGGGCAGGT-3' or 5'-
AGGCGTGGTGCGAGGCGGT-3'), to be used as tester.
Subtraction was performed using the Clontech PCR Select
CDNA subtraction kit. Pool of two schizophrenics, male age
44 and female age 56 (S-116, S-118) subtracted by pool of
two mentally normal male individuals ages 41 and 53
(S-124, S-141). Tissues were obtained from the Stanley
Neuropathology Consortium (www.stanleylab.org). Library
constructed and subtracted by Dr. Nancy Johnston [(410)
614-3918, nlj@welchlink.welch.jhu.edu]."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Peccora; Bovidae; Bovinae; Bos.

1 (bases 1 to 600)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.B. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross anatch v0.990329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD+3/332 600 bp mRNA linear 714674 MARC 6BOV Bos taurus CDNA 5', mRNA sequence. CB457332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6%; Score 27; DB 1;
100.0%; Pred. No. 0.085;
tive 0; Mismatches 0
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Seg primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="MARC 6BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled"
/lab_host="DH108"
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Best Local Similarity 100.0
Marches 27; Conservative
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VERSION
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LOCUS
DEFINITION
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PEATURES

ORIGIN

TITLE

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CX067711 733 bp mRNA linear EST 03-JAN-2005 1322352 NCCCWA 04RT Oncorhynchus mykiss cDNA, mRNA sequence. CX067711
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Rexroad,C.E., Rise,M., Koop,B., von Schalburg,K. and Yao,J. GRRY grool, NCCCWA/WVU EST Project, Phase II, in collaboration with GRASP
                                                                                                                                                                                                                                                                                       AL718806 AL718806 AL718806 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA Clone BNOAA037ZE05 3', mRNA sequence.
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1 (bases 1 to 609)

2 (colmbra, W. Well, D., Brottler, P., Blanchard, S., Levi, M., Hardellin, J. P., Weissenbach, J. and Perit, C. A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="inner_ear"
/dev_stage="embryonic"
/clone_lib="Danio_rerio_embryonic_inner_ear_subtracted
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Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
Gaps
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Oncorhynchus mykiss
                                                                1132 GACTCATCCTTCCAGGGCACCGACACA 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA037ZE05"
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Indels

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27; Conservative
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Matches 2
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    Matches
                                                                                                                                                  RESULT 70
DN615123/c
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AUTHORS
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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BF043991
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                                                           Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
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                                                                                                                                                                                                                                                                                            /lab host="Took...ozz."
/lab host="Took...ozz."
/clone_lib="NCCCWA 04RT"
/clone_lib="NCCCWA 04RT"
/note="Vector: pCR 4-TOPD. This is an early neurogenesis SSH library created by Mathew L. Rise constructed by subtracting late neurogenesis (mixed stages: hindbrain swelling + heart tube with peristalsis) from early neurogenesis (mixed stages: neural groove + 1/2 epiboly). Fish were from a domesticated strain (Spring Valley Trout Farm, Langley, B.C.), courteey of Bob Devlin, DFO. These are mostly internal (coding) sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes; Cyprinidae, Danio.

(bases 1 to 738)

(colmbra, W. Well, D., Brottier, P., Blanchard, S., Levi, M., Hardellin, J. P., Weissenbach, J. and Perit, C.

A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Danio rerio"
/mol_type="mRNA"
/db xref="taxon:7955"
/clone="BNOAAO25zB11"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 733;
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100.0%; Pred. No. 0.088;
tive 0; Mismatches 0; Indels
    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rerio cDNA clone BN0AA025ZB11 3', mRNA sequence.
  Kearneysville, WV 25430,
                                                                                                                                                                                                                                    organism="Oncorhynchus mykiss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="subtracted cDNA library"
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                                                                                                                                                Plate: 106 row: I column: 19
Seg primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:8022"
11876 Leetown Road, Kean
Tel: 304 724 8340 x2129
Fax: 304 725 0351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL717228.1 GI:20181831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio (zebrafish)
Danio rerio
                                                                                                                              cross_match v0.990329.
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Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Conservative
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Best Local Similarity
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AL717228/c
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KEYWORDS
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Query Match 1.6%; Score 27; DB 1; Best Local Similarity 100.0%; Pred. No. 0.088;

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/clone="PSCACI3"
//ida host="Mnole embryos excised from megagametophytes"
/lab host="Mnole"
/lab host="Mnole"
/clone lib="Subtracted pine embryo library, Lib B"
/clone lib="Subtracted pine embryo library, Lib B"
/clone lib="Subtracted pine embryo soricity bases of lobioly pine embryo site libeary enriched in
transcripts present in early phase of lobiolly pine embryo maturation. A subtractive library was made using the protocols of Clontech (Palo Alto,CA). RNA from lobiolly pine embryos in which cotyledons had just emerged (Stage 9.1, see Clavatta VT, Morillon R, Pullman GS, Chrispeels M, Cairney J. 2001. An aquaglyceroporin is abundantly expressed early in the development of the suspensor and the embryo proper of lobiolly pine (Pinus taeda L.). Plant Physiol. 127: 1556-1567
[http://www.plantphysiol.org/cgi/content/full/127/4/1556])
was subtracted from RNA from pine embryos collected two weeks after cotyledon emergence (Stage 9.3)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 bp mRNA linear EST 10-OCT-2000 BP250022B20H1 Soares normalized bovine placenta Bos taurus CDNA Glone BP250022B20H1 5', mRNA sequence.
                                                                                                                                                                                                                                                                                         EST 21-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: C. Robin Buell
Plant Genomics Group
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seq primer: M13 forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Buell, C.K., Zheng, L., Cowles, A. and Cairney, J.

Sequencing of ESTs from loblolly pine embryonic libraries
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                    EST968173 Subtracted pine embryo library, Lib_B Pinus taeda cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .768
/organism="Pinus taeda"
/mol_type="mRNA"
/cultivat="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
      Gape
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100.0%; Pred. No. 0.088;
ive 0; Mismatches 0; Indels
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                                                                  1687 TIGIAAGIACCICGGCCGCGACCACGC 1713
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EST 26-NOV-2002
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1 (bases 1 to 232)
Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G. 
Expressed sequence tags from soybean root hair subtractive cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.
Miao, G., Caraher, N. and Hanafey, M.K.
Unbublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
I Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2607
Pax: 302-631-2607
Email: Scott. V. Tingey@USA.dupont.com
Seq prime: T7.
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                                                                                                                                                                                                                                                                                                                                                                                                           /tisaue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: root hairs; Vector: pGEM-T-Easy; cDNA of generated from soybean root hair tissue treated with Bradyrhizobium japonicum for 6 hours."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 1.5%; Score 26; DB 7; Length 216; 1 Similarity 100.0%; Pred. No. 0.25; 26; Conservative 0; Mismatches 0; Indels
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                                                                                       Contact: Gary Stacey
University of Missouri
University of Missouri
University of Missouri
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wri2s.pk008.e13.f"
/tissue_type="leaf"
/lab_host="DH108"
/clone_lib="wri2s"
                                                                                                                                                                                                                                                                                              1. 216
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
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Triticum aestivum
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                                                                  Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                     Tel: 217 313 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Funding for cattle BST sequencing was provided by the USDA National

Foreign and the sequencing was provided by the USDA National

Foreign and Televin and J. E. Womack. Base Calling/Quality Scores: PHRED

from Washington University Genome Center. Vector Trimmi g:

Cross match from Washington University Genome Center PHRAP suite.

This sequence is vector free and at least 200 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Bex="female"
| Tab host="DHIOB" |
| Alab host="DHIOB" |
| Alab host="DHIOB" |
| Alab host="Organ: placenta; Vector: pT713Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contrributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6 (9): 791-806. "
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Bocora; Bovidae; Bovinae; Bos.
1 (bases 1 to 206)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
                                                                                                                                                                                                                                                                       Contact: Lewin, H. A. W. Keck Center for Comparative and Functional Genomics University of 111inois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 206 Std Error: 0.00
Plate: BP250022B20 row: H column: 1
Seq primer: AGCGGATAACAATTCACAGGA
High quality sequence stop: 206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9913"
/clone="BP250022B20H1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bos taurus"
  GI:10761046
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Unpublished (2000)
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                                               Bos taurus (cow)
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  BF043991.1
                                                                       Bos taurus
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IMAGE22035800, mRNA sequence.
                                                                                                                                                                                                                                                           AL726074 2020 DEST 18-APR-2002 AL726074 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA clone BN0AA080ZD03 5', mRNA sequence.
AL726074
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1 (Dases 1 to 255)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., Hardelin,J.P., Weissenbach,J. and Petit,C.

8 subtracted cDNA library from the zebrafish (Danio rerio) embryonic inner ear Unpublished (2002)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 288)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stāgē="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
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                                                                                            Gaps
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                      Length 232;
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                                                    Score 26; DB 6;
Pred. No. 0.26;
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comparable uninfected leaves"
                                          1.5%; Scc...
100.0%; Pred. No. v...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="inner ear"
                                                                                                                               1688 TGTAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                        205 TGTAAGTACCTCGGCCGCGACCACGC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 TGTAAGTACCTCGGCCGCGACCACGC 4
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                                                                                                                                                                                                                                                                                                                                 AL726074.1 GI:20190678
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                                                                                         26; Conservative
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                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Danio rerio
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                                                                                                                                                                                                                                                                                                                                                      EST
                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                           DEFINITION
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                                                                                         Matches
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AUTHORS
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KEYWORDS
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/downer="Invade: 201806"
/clone="Invade: 201806"
/tissue_type="frontal lobe (see description)"
/tissue_type="frontal lobe (see description)"
/lab host="DH108 (phage-resistant)"
/clone lib="Stanley Frontal SN pool 2"
/note="Organ: brain, Vector: pCR2.1-TOPO (Invitrogen);
Site_1: ECORI; Total RNA (purified with Trizol and DNAsed before use) was reverse transcribed using a modified oligo-dT primer containing Rsal and HindIII sites.
Double- stranded cDNA was digested with Rsal, resulting in blunt ended cDNA of an average 0.1-2 kb in length.
Digested cDNA was split into two sets, one used as is set the driver, the other set was split in half again and each half linked to a different adaptor
(5'-TCGAGCGCGCCGCGCGCGT-3'), to be used as tester.
Subtraction was performed using the Clontech PCR Select cDNA aubtraction kit. Pool of two schizophrenics, male age two mentally normal male individuals ages 41 and 53 (S-116, S-118) subtracted by pool of two mentally normal male individuals ages 41 and 53 (S-124, S-141). Tissues were obtained from the Stanley constructed and subtracted by Dr. Nancy Johnston [(410) 614-3918, nlj@welchlink.welch.jhu.edu]."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA734840 344 bp mRNA linear EST 26-NOV-2002 wpils.pk002.ell wpils Triticum aestivum cDNA clone wpils.pk002.ell 5' end, mRNA secuence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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1 (bases I to 344)

1 (bases I to 344)

1 (bases I to 344)

Mao, G., Caraher, N. Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Mao, G., Caraher, N. and Hanafey, M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
High quality sequence stop: 287,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
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CA734840
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ORIGIN

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Tumor Gene Index
Unpublished (1997)
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Best Local Similarity
Matches 26; Conserv
                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:1427458
                                                                                                                                           56;
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                   RESULT 78
BF150866
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1 (Dases I to 4082)

2 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Pahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle Genome Res. II (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                /clome_lib="wpils"
/note="Vector: PGEM-T Easy; Site_1: Smal; Wheat, Polk
cultivar (resistant), infected with septoria tritici
strain A 24 hours after infection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V. Tingey@USA.dupont.com
Seq primer: M13.
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                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 26; DB 6; Length 344;
100.0%; Pred. No. 0.27;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                            /organism="Triticum aestivum"
                                                                                                                                                                               /mol_type="mRNA"
db_xref="taxon:4565"
/clone="wpile.pk002.ell"
/tissue type="laf"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1688 TGTAAGTACCTCGGCCGCGACCACGC 1713
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/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reraderacercececescaces 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 18 row: G column: 24
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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LOCUS
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TITLE

COMMENT

45.

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425 bp mRNA linear EST 29-DEC-2000 uy89210.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666690 5', BP150866
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
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/dev_stage="7" months"
/dev_stage="7" months"
/dev_stage="7" months"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murojdea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 425)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sall; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                                 Gaps
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                                                                                                                                       1.5%; Score 26; DB 1; Length 402; ilarity 100.0%; Pred. No. 0.27; Conservative 0; Mismatches 0; Indels
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0.27;
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/Btrain="mix PNB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3666690"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 26; DB
llarity 100.0%; Pred. No. 0.2
Conservative 0; Mismatches
                                                                                                                                                                                                                                                      1295 GAAGCAGTGCCCACTCTGGCTCCTCC 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other ESTs: uy88g10.x1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .425
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -40RP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                   68 GAAGCAGTGCCCACTCTGGCTCCTCC
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EST 20-DEC-2002
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pGEM-T; suppressed subtract hybridizated cDNA prepared from rice callus mRNAs ligating to pGEM-T"
                                                                                                                                                                                                                                1. .475

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db xref="texon:10116"

/clone="srcs1-00007-e10"

/tissue type="Cornea"

/clone_lib="srcs1 (10883)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Site_2: EcoRI; rat corneas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECTION 485 bp mRNA linear EST 20-DEK SENTING SIGN SALING AND SALINA CDNA, MRNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/cul_tivar="Muyunjing No. 7"
/cul_dxref="xxxon:4530"
/clone_lib="Rice callus and differential tissue SSH
                                                                                                              Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00007 row: e column: 10.
Location/Qualifiers
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100.0%; Pred. No. 0.28;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 1.5%; Score 26; DB 6; Length 475; 1. Similarity 100.0%; Pred. No. 0.27; 26; Conservative 0; Mismatches 0; Indels
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Du,X., Wang,D. and Yang,J.
Rice cDNA from callus (2002)
Unpublished (2002)
Contact: DU Xiling
Institute of Genetics, Fudan University
Handan Road 220, Shanghai 200433, China
Tel: 86-21-6564-3715
Email: dxiling@yahoo.com.cn.
Location/Qualifiers
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/organism="Oryza sativa"
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1 (bases 1 to 475)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
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Matches 26; Conserv
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Matches 26, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Henniqhausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="tumor, gross tissue"
/dev stage="10 months"
/lab_host="bullo"
/lab_host="bullo"
/clone_lib="NCI_CGAP_Mam3"
/clone="forgan: mammarry; vector: pCMV-SPORT6; Site 1: SalI;
/incte="forgan: mammarry; vector: pCMV-SPORT6; Site 1: SalI;
/site 2: NotI, Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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                                                  AW762557 426 bp mRNA linear EST 04-MAY-2000 ur57f12.yl NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3154415 5',
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                                                                                                                                                                                                               Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Sukaryota: Metazota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                      1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Other ESTB: ur57f12.x1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487 GATGTTAAGCTCAAAGGCATCCCTGT 512
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High quality sequence stop: 422.
Location/Qualifiers
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                                                                                                                                                                                       Mus musculus (house mouse)
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CB732455.1 GI:29799612
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                                                                                                nRNA sequence.
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                                                                   DEFINITION
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CB732455
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Homo sapiens (human)
Homo sapiens
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AI267373/c
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                                    CP036397 501 bp mRNA linear EST 17-JUL-2003
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                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. 1 (bases 1 to 501) Genoplante.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (Dases 1 to 520)
Coimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J. and Petit, C.
A subtracted CDNA library from the zebrafish (Danio rerio) embryonic inner ear
                                                                                                                                                                                                                                                           Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                       This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 1.5%; Score 26; DB 6; Length 501; 1 Similarity 100.0%; Pred. No. 0.28; 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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/mol_type="mRNA"
/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4577"
/clone="QCG30h07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="embryo"
/clone_lib="QCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
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/cultivar="F2"
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Danio rerio
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RESULT 82
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7.7

Committee and the second

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/clone="INAGE:2035696"
/(issue type="frontal lobe (see description)"
/lab_host="Number frontal lobe (see description)"
/lab_host="Number frontal lobe (see description)"
/lab_host="Stanley Frontal SN pool 2"
/clone lib="Stanley Frontal SN pool 2"
/clone lib="Stanley Frontal SN pool 2"
/note="Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
Site_il EcoR1; Total RNA (purified with Trizol and DNAsed before use) was reverse transcribed using a modified oligo-dT primer containing Real and HindIII sites.
Digo-dT primer containing Real and HindIII sites.
Double stranded cDNA was digested with Rsal, resulting in blunt ended cDNA was split into two sets, one used as is as the driver, the other set was split in half again and each half linked to a different adaptor
(s-rccAAGCGGCCGCGCAAGGT-3' or 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 543)

14 (bases 1 to 543)

15 (bases 1 to 543)

16 (bases 1 to 543)

17 (bases 1 to 543)

18 (bases 1 t
                                     /tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality; sequence stop: 437.
Location/Qualifiers
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IMAGE:20135696, mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 520;
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                                                                                                                                                                                                                                                                                              /note="subtracted cDNA library
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1.5%; Score 26; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches
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/organism="Homo sapiens"
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/clone="BN0AA048ZB03"
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DRIGIN

CB464871/c LOCUS

RESULT 85

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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AL714414 Amio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA Danio rerio cDNA Clone BNOAA005ZH12 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 557)
Coimbra, R. Weil, D., Brottier, P., Blanchard, S., Levi, M.,
Hardelin, J.P., Weissenbach, J. and Petit, C.
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Unpublished (2002)
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
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/clone_lib="Danio rerio embryonic inner ear subtracted
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Contact: Genoscope
Contact: General Actional de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                             Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

(Cypriniformes; Cyprinidae; Danio.

(Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., Hardelin,J.P., Weissenbach,J. and Perit,C.

a wubrracted cDNA library from the zebrafish (Danio rerio) unpublished (2002)
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.00.0%; Pred. No. 0.28;
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1 (Bases I to 547)

Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries UNDA, ARS, US Meat Animal Research Center
Po Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Pax: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
trimmed with the aid of the trim_alt option. Vector identified with
plate: LAM8004 row: M column: 8
Seq primer: TAGAAGGCACAGTCGAGG.
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AL714240 GI:20178843
EST. EST. 18-APR-2002
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constructed and subtracted by Dr. Nancy Johnston [(410) 614-3918, nlj@welchlink.welch.jhu.edu]."
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/rolone lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tIssues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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726118 MARC 6BOV Bos taurus CDNA 3', mRNA sequence.
CB464871
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                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                             26 TGTAAGTACCTCGGCCGCGACCACGC 1
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AL716984 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA clone BNOAA021ZAO1 5', mRNA sequence.
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1 (bases 1 to 572)
2 (colmbra, W. Well, D., Brottier, P., Blanchard, S., Levi, M., Hardellin, J. P., Weissenbach, J. and Perit, C. A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                        /organism="Danio rerio"
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/clone="lib="Danio rerio embryonic inner ear subtracted
CDNA"
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/tissue_type="inner ear"
/dev stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
           Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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2 rue Gaston Gremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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1.5%; Score 26; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches
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                                                                                                     1. .561
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1 (Dases 1 to 558)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., Hardelin,J.D., Weissenbach,J. and Petit,C.
A subtracted CDNA library from the zebrafish (Danio rerio)
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( tases I to 561)

Loimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio)
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/clone_lib="Danio rerio embryonic inner ear subtracted
                                  Gaps
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                0; Indels
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             Pred. No. 0.28;
100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BNOAA005ZH12"
/tissue_type="inner ear"
                                                                          1688 TGTAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1688 TGTAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                          531 TGTAAGTACCTCGCCGCGACCACGC 556
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Unpublished (2002)
Contact: Genoscope
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      Best Local Similarity 100.
Matches 26; Conservative
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Fax: 81-45-50.9216

Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Pukuda,S., Hashizume,W., Hayashida,K., Hizozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kadawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Salto,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Warahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequence Mam. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia real-time sequence Science Laboratory in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yanar, Z., Zavolan, M., Zhu, Y., Zimer, A., Yanagisawa, M., Yang, L., Yanar, Z., Zavolan, M., Zhu, Y., Zimer, A., Zhu, M., Makamura, M., Bakarume, N., Sato, K., Shiraki, T., Konno, H., Nakamura, M., Arakwa, T., Kukuda, A., Harahizume, W., Imotani, K., Ishii, Y., Arakwa, T., Yukuda, A., Harahizume, W., Imotani, K., Ishii, Y., Shinagawa, A., Yasunishi, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/strain="C57BL/6J"
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1 (Dases 1 to 657)

2 (Cazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Golobori,T., Baldarelli,R., Hill,D.P., Bult,C., Rohothia,C., Corbani,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.B., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gustinoich,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pescle,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachadran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reingle,R.D., Tomita,M., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
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                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. (basee 1 to 581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
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                2CU9g04.yg QCU Zea mays cDNA clone QCU9g04, mRNA sequence.
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93, rue Henri Rochefort 91025 EVRY CEDEX France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="seedling minus kernel"
/clone Tib="QCU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 1.5%; Score 26; DB 6;
Local Similarity 100.0%; Pred. No. 0.28;
nes 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Zea mays"

mol type="mRNA"

/cultivar="f333 or f334"

/db xref="taxon:4577"

/clone="QCU9904"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:5341085"
/clone="IMAGE:5341085"
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/dev stage="tumor, gross tissue"
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
/site 2: Not!; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                                                                                                                                                                                                                                 E 1 (bases 1 to 680)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inh.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11866 row: g column: 06

High quality sequence stop: 676.
BI653517 680 bp mRNA linear EST 12-SEP-2001
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602903535F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5033097 5',
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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100.0%; Pred. No. 0.28;
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
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Matches 26; Conservative 0; Mismatches
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                                                                                                                                      Mus musculus (house mouse)
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                                                                                             BI653517.1 GI:15567753
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BI156000
                                                  mRNA sequence.
                                                                                                                                                                  Mus musculus
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Cramer, R.A., Craven, K.D., Thon, M.R., Cho, Y., Knudson, D.L., Mitchell, T.K. and Lawrence, C.B.
Expressed Sequence Tag (BST) Analysis of a Compatible Alternaria brassicicola-Brassica oleracea Interaction
Unpublished (2005)
Contact: Dr. Thomas K. Mitchell
Contact: Dr. Thomas K. Mitchell
Contact: Dr. State University
B51 Main Campus Dr. Suite 233, Raleigh, NC 27606, USA
Tel: (919) 513-024
Fax: (919) 513-024
Email: thomas mitchell@ncsu.edu
Seq primer: T7 SP6 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="NCI CGAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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Alternaria brassicicola
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pGEMt; Mycelia Culture grown for 48 hours,
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D. cDNA Library Preparation: Life Technologies, Inc. cons. Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Phttp://image.lnll.gov
Plate: LLAMI1092 row: f column: 10
High quality sequence stop: 685.
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/clone_lib="A. brassicicola mycelial culture infecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="tumor, gross tissue"
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/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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/db xref="taxon:10090"
/clone="IMAGE:5033097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.2 Matches 26; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                   CV943849 1707 bp mRNA linear EST 25-JAN-2005 PU003E7 mycelium, subtracted infection mimic Phytophthora infestans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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24 degrees C, minimal media minus Nitrogen. Infecting
Brassica oleracea Var. Capitata cultivar 'tendersweetFl'"
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Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
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/note="Vector: pSPORT1"
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15782637
Contact: Judelson HS
                                                                          Length 692;
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/mol_type="mRNA"
/strain="88069"
                                                                          1.5%; Score 26; DB 8;
100.0%; Pred. No. 0.29;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers
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                                                                                                                                                                      28 TGTAAGTACCTCGGCCGCGACCACGC 3
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EST.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                 CDNA, mRNA sequence.
                                                                                           Local Similarity 100.
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1284 row: e column: 05
High quality sequence stop: 720.
I. 722
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Glirospathi; Muroidea; Murinae; Mus.

1 (bases 1 to 722)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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PU011H10 mycelium, subtracted infection mimic Phytophthora
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100.0%; Pred. No. 0.29;
ive 0; Mismatches 0; Indels
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Phytophthora infestans
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CV944323.1 GI:58134079
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Gaps

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
DDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1642 row: o column: 20
High quality sequence stort: 3
High quality sequence stop: 746.
Location/Qualifiers
      Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                                                               BI905713 746 bp mRNA linear EST 16-OCT-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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1.5%; Score 26; DB 3; Length 746;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                            Length 746;
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0.29;
                                                                                         1.5%; Score 26; DB
100.0%; Pred. No. 0.2
:ive 0; Mismatches
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/organism="Mus musculus"
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/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:5254507"
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Best Local Similarity 100.09
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BI905713
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmaliais Eutheria; Euarchoncoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 746)

RS NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Nubblished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbbs-romail.nih.gov

Tissue Procurement: Lochar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

Plate: LLAM11162 row: a column: 07

High quality sequence start: 3

High quality sequence start: 3

Location/Qualifiers
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/tissue_type="tumor, gross tissue"
/tasue_type="tumor, gross tissue"
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/lab_host="nullo"
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/note="forgan: māmmary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: NotI; Cloned unidirectionally. Primer: Ōligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
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/note="Vector: pSPORT1"
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    Plant-Microbe Interact. 18 (3), 229-243 (2005)
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100.0%; Pred. No. 0.29;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       /organism="Phytophthora infestans"
                                                                                                              USA
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
Mol. Plant-Microbe Interact. 18 (3), 15782637
Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, US
Tel: 909 787 4199
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/organism="Mus musculus"
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                                                                                                                                                                        Bmail: howard.judelson@ucr.edu
Location/Qualifiers
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/sex="A1"
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Sequence 8473,
Sequence 8150,
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                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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APPLICANT: Endege, Wilson O.
APPLICANT: Fordy Donna M.
APPLICANT: Schlegel, Robert
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TITLE OF INVENTION: ABE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
TITLE REPREBACE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
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APPLICANT: Ford, Donna M.
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APPLICANT: Schiegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENESA AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENESA AND GENE EXPRESSION PROSTATE CANCER
TITLE OF INVENTION: QUAZ.
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; Patent No. 6476207
                                                                                                                                                                                           104 AAGTACCTCGGCCGCGACCACGC 82
                                                                                                                                                                                                                                                                                                                                                                      US-09-328-475C-246/c
; Sequence 246, Application US/09328475C
; Patent No. 6476207
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// LOCATION: (1)...(483)
// OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-239

Query Match
Best Local Similarity 100.C
Matches 23; Conservative
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Best Local Similarity 100.
Matches 23; Conservative
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NAME/KEY: misc_feature
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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                                                                                                                                                                                           Sequence 8150, Application US/10131827

Sequence 8150, Application US/10131827

Sequence 8150, Application US/10131827

GENERAL INFORMATION:

APPLICANT: Woodward, Nobert

APPLICANT: Fry, Kirk

APPLICANT: Pry, Nace

APPLICANT: US, Nace

APPLICANT: US NOWBER: US 10/006,290

PRIOR APPLICATION NUMBER: US 10/006,290

PRIOR PILING DATE: 2001-10-22

PRIOR PILING DATE: 2001-06-08

PRIOR PILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 9090

SOFTWARE: Patentin Version 3.1

SEQ ID NO 9150
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Sequence 111, Application US/09328475C

Sequence 111, Application US/09328475C

Sequence 111, Application US/09328475C

Sequence 111, Application US/09328475C

Septicant: Applicant: Acted, John H.

APPLICANT: Acted, John H.

APPLICANT: Ford, Donna M.

APPLICANT: Schlegel, Wilson O.

APPLICANT: Schlegel, Robert

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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 111
LENGTH: 468
                                      GTAAGTACCTCGGCCGCGACCACGC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1691 AAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature; LOCATION: (1)...(170); OTHER INFORMATION: N = A, T, C or G US-10-131-827-8150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; LOCATION: (1)...(468)
COTHER INFORMATION: n = A,T,C or G
US-09-328-475C-111
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapien
                                                                                                                                                                               US-10-131-827-8150
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DB 3; Length 499; 0.61;

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Query Match
1.3%; Score 23; DB
Best Local Similarity 100.0%; Pred. No. 0.6
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                  1691 AAGTACCTCGGCCGCGACCACGC 1713
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(499)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapien
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Bradege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John B.
APPLICANT: Schiegel, Robert
APPLICANT: Schiegel, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSTATE CANCER
TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSTATE CANCER
TITLE OF INVENTION: APPLICATION NUMBER: US/09/328,475C
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: PASESEQ for Windows Version 3.0
SOFTWARE: PASESEQ for Windows Version 3.0
                                                                             Gaps
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APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathlen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REPRENENT: 153-002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
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1.3%; Score 23; DB 3; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels
                            Length 483;
                                                                        0; Indels
                       DB 3;
0.61;
                       1.3%; Score 23; DB 100.0%; Pred. No. 0.6 tive 0; Mismatches
                                                                                                                         1691 AAGTACCTCGGCCGCGACCACGC 1713
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US-09-128-475C-185/c
Sequence 185, Application US/09328475C
Patent No. 6476207
GENERAL INFORMATION:
                                                                                                                                                     104 AAGTACCTCGCCGCGACCACGC 82
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US-09-328-475C-224/c
S. Sequence 224, Application US/09328475C
; Patent No. 6476207
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-224
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
     Query Match
Best Local Similarity 100.0
...rhes 23; Conservative
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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Sequence 181, Application US/09328475C

Sequence 181, Application US/09328475C

Patent No. 4976207

GENERAL INFORMATION:
APPLICANT: Chang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Scinegal, Robert
APPLICANT: Steinmann, Vathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Wathleen E.
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APPLICANT: Zhang, Jimmy
APPLICANT: Astel, John
APPLICANT: Astel, John
APPLICANT: Bridge, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT PILLING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
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8-09-328-475C-196/c
; Sequence 196, Application US/09328475C
; Patent No. 6476207
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NAME/KEY: misc_feature
LOCATION: (1)...(501)
OTHER INFORMATION: n = A,T,C or G
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Gaps
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TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 277
LENGTH: 724
TYPE: DNA
ORGANISM: Homo Sapien
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 315
LENGTH: 722
TYPE: DNA
ORGANISM: Homo Sapien
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1.3%; Score 23; DB 3; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels
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; Sequence 277, Application US/09128475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Actel, Jon APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1691 AAGTACCTCGGCCGCGACCACGC 1713
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Patent No. 6476207
GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 AAGTACCTCGGCCGCGACCACGC 73
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NAME/KEY: misc_feature

LOCATION: (1)...(722)

OTHER INFORMATION: n = A,T,C or G
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| LOCATION: (1)...(724)

| OTHER INFORMATION: n = A,T,C or G

US-09-328-475C-277
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APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
**noT.TCANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-328-475C-295
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US-09-328-475C-305/c
| Sequence 305, Application US/09328475C
| Sequence 305, Application US/09328475C
| Patent No. 6476207
| GENERAL INFORMATION:
| APPLICANT: Zahaq, Jimmy |
| APPLICANT: Carroll III, Eddie |
| APPLICANT: Endege, Wilson O. |
| APPLICANT: Ford, Donna M. |
| APPLICANT: Schlegel, Robert |
| AP
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APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Nobert
APPLICANT: Schlegel, Robert
APPLICANT: Stellmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
                                                                                                                                                                                                                                                                                                                                                                       Length 511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.3%; Score 23; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches
             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 196 LENGTH: 511
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10.99-328-315, Application US/09328475C

5 Patent No. 6476207

5 GENERAL INFORMATION
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COTHER INFORMATION: n = A,T,C or G
US-09-328-475C-305
                                                                                                                                                                                                                                         ; LOCATION: (1). T. (511)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-196
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Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
                                                                                                            TYPE: DNA
ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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APPLICANT: Ascel, Jonmy
APPLICANT: Ascel, Jon H.
APPLICANT: Bridge, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ASE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SERGIF OF THE TENDER OF THE T
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1.3%; Score 23; DB 3; Length 727;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(727)
CTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(736)
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Bridge, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen B.
TITLE OF INVENTION: GREES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIPPERENTIALLY REGULATED IN PROSTATE CANCER
FILE REPERBNCE: 1532.002/200130.463
CURRENT PELING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NOS: 341
SEQ ID NO 329
LIGHTH: 725
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                                                APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John B.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REPERENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 295
LENGTH: 725
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:ive 0; Mismatches
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; Sequence 329, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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US-09-328-475C-331/c
; Sequence 331, Application US/09328475C
; Patent No. 6476207
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; LCCATION: (1)...(725)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-295
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LOCATION: (1)...(725)

CTHER INFORMATION: n = A,T,C or G

US-09-328-475C-329
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Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapien
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Matches
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Gaps ö

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                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.

APPLICANT: Carroll III; Eddie
APPLICANT: Budege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Mondan, John E.

APPLICANT: Steinman, Kathleen E.

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: QUARER 1999-06-09

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SEQ ID NO 294

LENGTH: 736
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Sequence 294, Application US/09328475C Patent No. 6476207
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APPLICANT: MONDAIN M.
APPLICANT: MONDAIN M.
APPLICANT: MONDAIN M.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: PASSES for Windows Version 3.0
SEQ ID NO 276
LENGTH: 744
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US-09-328-475C-276/C
is Sequence 276, Application US/09328475C
is Patent No. 6476207
is GENERAL INFORMATION:
is APPLICANT: Abrang, Jimmy
is APPLICANT: Abrang, Jimmy
is APPLICANT: Abrang, Jimmy
is APPLICANT: Carroll III, Eddie
is APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1691 AAGTACCTCGGCCGCGACCACGC 1713
          1691 AAGTACCTCGGCCGCGACCACGC 1713
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                                                                         124 AAGTACCTCGGCCGCGACCACGC 102
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; Sequence 330, Application US/09328475C
; Patent No. 6476207
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ORGANISM: Homo Sapien
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(744)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(741)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.C
Matches 23; Conservative
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ORGANISM: Homo Sapien
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GENERAL INFORMATION:

APPLICANT: Astel, Jon H.

APPLICANT: Astel, Jon H.

APPLICANT: Endege, Wilson O.

APPLICANT: Endege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Ford, Donna M.

APPLICANT: Schlegel, Robert B.

APPLICANT: Robert B.

APPLIC
                                                                                                                                                                        APPLICANT: Carrol III. Eddie
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carrol III. Eddie
APPLICANT: Carrol III. Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 314
LENGTH: 740
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100.0%; Pred. No. 0.61;
.ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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RESULT 18
US-09-328-475C-314/C
; Sequence 314, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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US-09-328-475C-304/c
; Sequence 304, Application US/09328475C
; Patent No. 6476207

; LOCATION: (1)...(740)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-314

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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 23; Conservative
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Best Local Similarity 100.
Matches 23; Conservative
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GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy
APPLICANT: Actal, Jon H.
APPLICANT: Actal, Jon H.
APPLICANT: Badege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE
CURRENT PAPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 330
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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Sequence 268, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith B.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
PILE REPERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SSOFTWARE: PatentIn Ver. 2.0
IENGTH: 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Achiegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 153
SEQ ID NO 153
LENGTH: 780
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                                                                                                                                                                          DB 3; Length 772; 0.61;
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0.61;
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                                                                                                                                                                        Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-328-475C-153/c; Sequence 153, Application US/09328475C; Patent No. 6476207; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         86 AAGTACCTCGGCCGCGACCACGC 64
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                                                                     ; LOCATION: (1)....(772)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-158
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| LOCATION: (1)...(780)

| OTHER INFORMATION: n = A,T,C or G

US-09-328-475C-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
                                                 NAME/KEY: misc_feature
LOCATION: (1)...(772)
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ORGANISM: Homo Sapien FEATURE:
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US-09-328-475C-158/C
i Sequence 158, Application US/09328475C
j Patent No. 6476207
i GENERAL INFORMATION:
i APPLICANT: ZAnag, Jimmy
i APPLICANT: Carroll III, Eddie
j APPLICANT: Endes, Wilson O.
APPLICANT: Endes, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, ART DIFFERENTIALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE
TITLE OF SEQ ID NOS: 341
CURRENT APPLICATION NUMBER: 1959-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 158
SEQ ID NO 158
LENGTH: AVED.
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Steinman, Kathleen E.
TITLE OF INVENTION: GRENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GRENES AND GENE EXPRESSION PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT PILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Pred. No. 0.61;
                                                   1.3%; Score 23; DB 3; Length 744;
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                                                                             0.61;
                                            Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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US-09-328-475C-328/C
; Sequence 328, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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LOCATION: (1)...(747)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo Sapien
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Matches 23; Conserv
US-09-328-475C-276
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LENGTH: 747
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 229 LENGTH: 815
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Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapien
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US-09-328-475C-167/C

Sequence 167, Application US/09328475C

Sequence 167, Application US/09328475C

Sequence 167, Application US/09328475C

Sequence 167, Application US/09328475C

GENERAL INFORMATION:
APPLICANT Astel, Jonn
APPLICANT Garcoll III, Eddie
APPLICANT Carroll III, Eddie
APPLICANT Schlege, Wilson O.
APPLICANT Schlegel, Robert
APPLICANT Steinmann, Kathleen E.
APPLICANT STEINMANN STEINMANN STEINMANN VARIEN STEINMANN VARIE
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US-09-328-475C-229/C
is Sequence 229, Application US/09328475C
is Patent No. 6476207
is GENERAL INFORMATION:
is APPLICANT: Zahag, Jūmmy
is APPLICANT: Astel, Jon H.
is APPLICANT: Endege, Wilson O.
is APPLICANT: Ford, Donna M.
is APPLICANT: Schlegel, Robert
is APPLICANT: Sthemann, Kathleen E.
is APPLICANT: Sthemann, Kathleen E.
is APPLICANT: Stelmann, Kathleen E.
is APPLICANT: Stelmann, ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
is TILE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
is TILE OF INVENTION: 48199-06-09
is CURRENT FILING DATE: 1999-06-09
is NUMBER OF SEQ ID NOS: 341
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100.0%; Pred. No. 0.61;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                Length 781;
                                                                                                                                                                                                                                DB 3;
0.61;
                                                                                                                                                                                                                                Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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                                       NAME/KEY: misc feature
LOCATION: (1)...(781)
OTHER INFORMATION: n = a, t, c or g
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OTHER INFORMATION: n = A,T,C or G
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Matches 23; Conservative
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ORGANISM: Homo Sapien
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APPLICANT: Zhang, Jimmy
APPLICANT: Zhang, Jimmy
APPLICANT: Carroll III, Eddie
APPLICANT: Batel, Jon H.
APPLICANT: Bridge, Wilson O.
APPLICANT: Bridge, Wilson O.
APPLICANT: Bridge, Wilson O.
APPLICANT: Schlege, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE
TITLE OF INVENTION: 1999-06-09
CURRENT FILING DATE: 1999-06-09
CURRENT FILING DATE: 1999-06-09
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PastSEQ for Windows Version 3.0
SOFTWARE: BASE OF THE CARROLL AND THE 
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                      Query Match
1.3%; Score 23; DB 3; Length 815;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels
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APPLICANT: Zhang, Jimmy
APPLICANT: Carroll III, Eddie
APPLICANT: Badege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegell, Robert
APPLICANT: Schlegell, Robert
APPLICANT: Schlegell, Robert
APPLICANT: Sthlegell, Robert
APPLICANT: Sthlegell, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
                                                                                                                                                                                                                                                                                                                                                                                                  1691 AAGTACCTCGGCCGCGACCACGC 1713
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2-09-328-475C-249/c
; Sequence 249, Application US/09328475C
; Patent No. 6476207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 AAGTACCTCGGCCGCGACCACGC 60
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Patent No. 6476207
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NAME/KEY: misc_feature
NAME/TON: (1)...(815)
OTHER INFORMATION: n = A,T,C or G
LOCATION: (1)....(815)

COTHER INFORMATION: n = A,T,C or G
US-09-328-475C-229
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NAME/KEY: misc feature LOCATION: (1)...(829)
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ORGANISM: Homo Sapien
FEATURE:
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TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: RatSEQ for Windows Version 3.0
SEQ ID NO 249
LENGTH: 821
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1.3%; Score 23; DB 3; Length 821;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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US-09-328-475C-191/C
Sequence 191, Application US/09328475C
Patent No. 6476207
GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: AAtel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                        1691 AAGTACCTCGGCCGCGACCACGC 1713
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-249
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| LOCATION: (1)...(822)

| CTHER INFORMATION: n = A,T,C or G

US-09-328-475C-245
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NAME/KEY: misc_feature
                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
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Matches 23; Conserva
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Caracial III; Eddie
APPLICANT: Caracial III; Eddie
APPLICANT: Ford Donna M.
APPLICANT: Ford Donna M.
APPLICANT: Ford Donna M.
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
CURRENT FILLING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 255
LENGTH: 830
APPLICANT: Ford, Donna M.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

APPLICANT: Steinmann, Kathleen E.

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: FRAEKEN FOR 3.41

SOFTWARE: PRESENCE FOR WINGOWS VERSION 3.0

SEQ ID NO 191

LENGTH: 829

TYPE: DNA

ORGANISM: Homo Sapien
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1.3%; Score 23; DB 3; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels
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0.61;
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; Sequence 43, Application US/09328475C
; Patent No. 6476207
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US-09-328-475C-191
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US-09-328-475C-225
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TYPE: DNA
ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
                            US-09-328-475C-103/c
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Sequence 102, Application US/09328475C

Patent No. 6476207

GENERAL INFORMATION:

APPLICANT: Abrel, Jon H.

APPLICANT: Carroll III, Eddie

APPLICANT: Bendege, Wilson O.

APPLICANT: Bendege, Wilson O.

APPLICANT: Schiegel, Robert

APPLICANT: Schiegel, Robert

APPLICANT: Schiegel, Robert

APPLICANT: Schiegel, Robert

TITLE OF INVENTION: GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENE AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

FILE REPERENCE: 1532.002/200130.463

CURRENT APPLICATION NUMBER: US/09/328,475C

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

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                                                                      APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GRNES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER FILE REPERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 43
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(1020)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-43
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
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Best Local Similarity 100.
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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                                                                                                                                                                                         APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John B.
APPLICANT: Monahan, John B.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERRNTIALLY REGULATED IN PROSTATE CANCER
FILE REPERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastsEQ for Windows Version 3.0
ERNGTH: 1021
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APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1332.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 1024
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US-09-328-475C-51/C
is Sequence 51, Application US/09328475C
is Patent No. 6476207
is GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
Sequence 103, Application US/09328475C Patent No. 6476207
GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy APPLICANT: Astel, Jon H, APPLICANT: Carroll III, Eddie APPLICANT: Bndege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AAGTACCTCGGCCGCGACCACGC 79
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| NAME/KEY: misc feature | LOCATION: (1)...(1021) | COCATION: (1)...(1021) | COTER INFORMATION: n = A,T,C or G US-09-328-475C-103
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| LOCATION: (1)...(1024)
| OTHER INFORMATION: n = A,T,C or
US-09-328-475C-51
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Best Local Similarity 100.
Matches 23; Conservative
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Matches 23; Conservative
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GENERAL INFORMATION:

APPLICANT: Shang, Jimmy
APPLICANT: Actal, Jon H,
APPLICANT: Actal, Jon H,
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
CURRENT STANG DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 77
LENGTH: 1024
MUNDER OF SEQ ID NO 77
LENGTH: 1024
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APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.

APPLICANT: Astel, Jon H.

APPLICANT: Bndege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Sthlegel, Robert
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REPERBRÜCE: 1532.002/200130-463
CURRENT PILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 78

LENGTH: 1024
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
                                                                                                                                                       0; Indels
                                                                         DB 3;
                                                                     Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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; Patent No. 6476207
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NAME/KEY: misc_feature
LOCATION: (1)...(1024)
OTHER INFORMATION: n = A,T,C or G
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Matches 23; Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 39
US-09-328-475C-77/c
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US-09-328-475C-78
US-09-328-475C-71
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Astel, Jonn H.
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Mondan, John E.
APPLICANT: Stellegel, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
TURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOCTIARE: PESELSQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 1024
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Badege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GREENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GREENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: QREENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: QREENES AND GENE EXPRESSION PRODUCTS THAT
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                                    1691 AAGTACCTCGGCCGCGACCACGC 1713
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                                                                                 99 AAGTACCTCGGCCGCGACCACGC 77
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US-09-228-475C-56/C
Sequence 56, Application US/09328475C
Patent No. 6476207
GENERAL INFORMATION:
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US-09-328-475C-71/C
Sequence 71, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-56
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NAME/KEY: misc feature
LOCATION: (1): (1024)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo Sapien
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TYPE: DNA; ORGANISM: Myxococcus xanthus US-09-902-540-8302
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ORGANISM: Myxococcus xanthus
US-09-902-540-866
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Best Local Similarity 100.
Matches 23; Conservative
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US-09-902-540-8302
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US-09-902-540-866
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE
TITLE OF STWENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 93
SEQ ID NO 93
LENGTH: 1024
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US-09-328-475C-334
US-09-328-475C-334

| Sequence 334, Application US/09328475C |
| Patent No. 6476207 |
| GENERAL INFORMATION: |
| APPLICANT: Zhang, Jimmy |
| APPLICANT: Carroll III, Eddie |
| APPLICANT: Endes, Wilson O. |
| APPLICANT: Monahan, John E. |
| APPLICANT: Schlegel, Robert |
| TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT |
| TITLE OF INVENTION: ARE DIFFRERNITIALLY REGULATED IN PROSTATE CANCER |
| FILE REFERENCE: 1532.002/200130.463 |
| CURRENT APPLICATION NUMBER: US/09/328,475C |
| CURRENT FILING DATE: 1999-06-09
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Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches
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; Sequence 93, Application US/09328475C
; Datent No. 6476207
; GENERAL INFORMATION:
                                                NAME/KEY: misc_feature

| LOCATION: (1)...(1024)

| OTHER INFORMATION: n = A,T,C or G

US-09-328-475C-78
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-93
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ORGANISM: Homo Sapien
FEATURE:
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ORGANISM: Homo Sapien
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (13849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8302
LENGTH: 2253
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Steven C.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Mycococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10 (15649)8
CURRENT PLILING DATE: 2001-07-10
CURRENT FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 866
LENGTH: 6339
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100.0%; Pred. No. 0.61;
tive 0; Mismatches 0; Indels
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 2051
TYPE: DNA
; ORGANISM: Homo sapien
; FRATURE:
; LOCATION: (1) ... (2051)
; COTHER INFORMATION: n = A,T,C or G
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  Score 23; DB 3; Length 6339;
Pred. No. 0.61;
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleaman, Matthew
APPLICANT: Sleaman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOUTHARRE: FastSEQ for Windows Version 3.0
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
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                                             0; Indels
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Query Match 1.3%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 23; Conservative 0; Mismatches
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                                                                                                                              1190 GACCTGGACCTGCCGGAGATGG 1212
                                                                                        666 GGACCTGGACCTGCCGGAGATGG 688
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Matches 22; Conservative
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Best Local Similarity 100.
Matches 22; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mouse
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US-09-312-283C-4/c
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LENGTH: 311
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LENGTH: 311
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Sequence 200, Application US/09328475C
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 MS-09-328-475C-222/C

1 Sequence 222, Application US/09328475C

1 Sequence 222, Application US/09328475C

2 Sequence 222, Application US/09328475C

2 GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy

APPLICANT: Asteil, Jon H.

APPLICANT: Ford, Donna M.

APPLICANT: Ford, Donna M.

APPLICANT: Monahan, John E.

APPLICANT: Steinmann, Kathleen E.

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GABE EXPRESSION PROSTATE CANCER

TITLE OF INVENTION: APPLICANTON NUMBER: US/09/328,475C

CURRENT FILING DATE: 199-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: FastSEQ for Windows Version 3.0

SENGTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-194
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Squence 8248, Application US/10131827

Squence 8248, Application US/10131827

Squence 8248, Application US/10131827

GENERAL INFORMATION:

APPLICANT: Woolgemuth, Jay

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Ro
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                                                                      APPLICANT: Zhang,
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Actil, Jon H.
APPLICANT: Badege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Bronden, John E.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Rathleen E.
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION NUMBER: 1999-06-09
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 200
LENGTH: 506
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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1.3%; Score 22; DB 3; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature; LCCATION: (1)...(506); COTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.(
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
Patent No. 6476207
GENERAL INFORMATION:
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RESULT 53

RESULT 51 US-09-328-475C-200/c

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122 AGTACCTCGGCCGCGACCACGC 101
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
                                                                                                              RESULT 55
US-09-328-475C-169
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US-09-328-475C-280/C

i Sequence 260. Application US/09328475C

j Patent No. 6476207

i GENERAL INFORMATION:

i APPLICANT: Zahag, Jimmy

i APPLICANT: Carroll III, Eddie

APPLICANT: Endege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Prod, Donna M.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE

CURRENT APPLICATION WHERE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SEQ ID NO 280

SEQ ID NO 280

LENGTH. 751

TUBENTH: 751

TUBENTH: 751
                                                                                                                                                     APPLICANT: Carcol III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Stheman, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: ARE 1999-06-09
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 281
LENGTH: 727
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US-09-328-475C-281/C

Sequence 281, Application US/09328475C

Patent No. 6476207

GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy

APPLICANT: Astel, Jon H.

APPLICANT: Astel, Jon H.

APPLICANT: Endege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Mondann, John B.
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; OTHER INFORMATION: n = A, T, C or G
US-09-328-475C-281

', LOCATION: (1)...(751)
', OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-280

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapien
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US-09-328-475C-176/C

US-09-328-475C-176/C

Sequence 176, Application US/09328475C

Batent No. 6476207

GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy

APPLICANT: Carroll III, Eddie

APPLICANT: Endes, Wille Non H.

APPLICANT: Endes, Wille Non H.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

FILE REFERENCE: 1532.002/200130.463

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SEQ ID NO 176

SEQ ID NO 176

LENGTH: 773

TYDE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE

FILE REPERENCE: 1532.002/200130.463

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SEQ ID NO 176

LENGTH: 773

TYDE: NAN'A
                                                                                                                                                                                                  APPLICANT: Ford, John B.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 169
LENGTH: 771
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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; Sequence 169, Application US/09328475C; Patent No. 6476207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: Misc_feature
LOCATION: (1)...(771)
OTHER INFORMATION: n = A,T,C or G
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i_CCATION: (1)...(773)
CTHER INFORMATION: n = A,T,C or G
US-09-328-475C-176
                                                      GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
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Matches 22; Conservative
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NAME/KEY: misc_feature
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US-09-328-475C-168/C
is Sequence 168, Application US/09328475C
is Septent No. 6476207
is APPLICANT: Carroll III, Eddie
is APPLICANT: Asteil, Jon H.
is APPLICANT: Roadege, Wilson O.
is APPLICANT: Ford, Donna M.
is APPLICANT: Schlegel, Robert
is APPLICANT: Steinmann, Vachleen E.
is APPLICANT: Steinmann, Kathleen E.
is APPLICANT: Steinmann, Kathleen E.
is TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
iTITLE OF INVENTION: ABE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
is TILLE REPERENCE: 1532.002/200130.463
is CURRENT FILING DATE: 1999-06.09
is NUMBER OF SEQ ID NOS: 341
is SOFTWARE: FeatSEQ for Windows Version 3.0
is SEQ ID NO 168
is LENOTH: 780
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Brdege, Wilson O.
APPLICANT: Brdege, Wilson O.
APPLICANT: Schlegel, Robert
CURRENT APPLICATION INDMER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 163
LENGTH: 776
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1.9;
DB 3; Length 773;
1.9;
                                                    0; Indels
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Query Match 1.3%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 1.9 Matches 22; Conservative 0; Mismatches
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                                                                                                       1692 AGTACCTCGGCCGCGACCACGC 1713
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Sequence 163, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
                                                                                                                                                    86 AGTACCTCGGCCGCGACCACGC 65
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-163
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LOCATION: (1)...(776)
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jonny
APPLICANT: Astel, Jonny
APPLICANT: Astel, Jonny
APPLICANT: Redee, Wilson O.
APPLICANT: Rodes, Wilson O.
APPLICANT: Rodes, Wilson O.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, John
APPLICANT: Schlegel, Joh
APPLICANT: Schlegel, John
APPLICANT: Schlegel, John
APPLICANT: J
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APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Schiegel, Robert
APPLICANT: Steinman, Rahleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FASTERQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                     1.3%; Score 22; DB 3; Length 780;
100.0%; Pred. No. 1.9;
trive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1692 AGTACCTCGGCCGCGACCACGC 1713
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8-09-328-475C-119/c
; Sequence 119, Application US/09328475C
; Patent No. 6476207
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; LOCATION: (1)...(780)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-168
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OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.(
Matches 22, Conservative
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Matches 22; Conservative
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NAME/KEY: misc_feature
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APPLICANT: Changy, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Gracial III, Eddie
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Stelmann, Kathleen B.
ITILE OF INVENTION: GRASS AND GENE EXPRESSION PRODUCTS THAT
ITILE OF INVENTION: GRASS AND GENE EXPRESSION PROSUCTS THAT
ITILE OF INVENTION: GRASS AND GENE EXPRESSION PROSUCTS THAT
ITILE OF INVENTION: GRASS AND GENE EXPRESSION PROSUCTS THAT
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1.9;
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; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 195
; LENGTH: 848
TYPE: DNA
; ORGANISM: Homo Sapien
; FRATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(848)
; COTTER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.3%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 1.9 Matches 22; Conservative 0; Mismatches
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1.3%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 22; Conservative 0; Mismatches
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; Sequence 57, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-104
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Endege, Wilson O.
Ford, Donna M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
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APPLICANT:
APPLICANT:
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Budege, Wilson O.
APPLICANT: Bndege, Wilson O.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER;
FILE REPERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 223
LENGTH 822
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US-09-328-475C-195/c
is Sequence 195, Application US/09328475C
is Patent No. 6476207
is GENERAL INFORMATION:
is APPLICANT: Zhang, Jimmy
is APPLICANT: Astel, Jon H.
is APPLICANT: Endese, Wilson O.
is APPLICANT: Pord, Donna M.
is APPLICANT: Schlegel, Robert
is APPLICANT: Schlegel, Robert
is APPLICANT: Schlegel, Robert
is APPLICANT: Schlegel, Robert
is APPLICANT: Steinmann, Kathleen E.
is APPLICANT: Steinmann, Kathleen E.
is TITLE OF INVENTION: GENER AND GENE EXPRESSION PRODUCTS THAT
it TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
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1.3%; Score 22; DB 3; Length 815;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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                                                                                                                                                         NAME/KEY: misc_feature; LOCATION: (1)...(815)
US-09-328-475C-238
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OTHER INFORMATION: n = A,T,C or G
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nes 22; Conservative
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                                                               TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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   SEQ ID NO 238
LENGTH: 815
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                                                                                                                                  FEATURE:
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APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathlen
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 57
LENGTH: 1024
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                                                                                                                                                                                                                                                                                                              Query Match 1.3%; Score 22; DB 3; Length 1024; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       103 AGTACCTCGGCCGCGACCACGC 82
                                                                                                                                                                                                                    FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(1024)

OTHER INFORMATION: n = A,T,C or G
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OTHER INFORMATION: n = A, T, C or G
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Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                      ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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                                                                                                                                                                                       TYPE: DNA
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RESULT 66
US-09-328-475C-62/c
S-09-328-475C-62/c
; Sequence 62, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:

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| Sequence 6.5 Application US/09328475C
| Patent No. 6476207
| GENERAL INPORMATION:
| APPLICANT: Zhang, Jimmy
| APPLICANT: Astel, Jon H.
| APPLICANT: Redege, Wilson O.
| APPLICANT: Ford, Donna M.
| APPLICANT: Schlegel, Robert
| APPLICANT: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
| TILLE OF INVENTION UNDER: 1999-06-09
| NUMBER OF SEQ ID NOS: 341
| SEQ ID NO 65
| EMOTH: APPLICANT: NUMBER OF SEQ ID NO 65
| EMOTH: NUMBER OF SEQ ID NOS: 341
| TILLE OF INVENTION UNDER: Schlegel, Robert
| TILLE OF INVENTION UNDER: Schlegel, Robert
| SEQ ID NO 65
| SEQ ID NO 65
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                                                                                                                  APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegell, Robert
APPLICANT: Schlegell, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION: ARE DIFFERENTALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION: ARE DIFFERENTALLY REGULATED IN PROSTATE CANCER
TITLE OF INVENTION WIMBER: US/09/328,475C
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 62
LENGTH: 1024
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1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Homo Sapien
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(1024)
CTHER INFORMATION: n = A,T,C or G
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i_CCATION: (1)...(1024)
cOTHER INFORMATION: n = A,T,C or G
US-09-328-475C-65
Zhang, Jimmy
Astel, Jon H.
Carroll III, Eddie
Endege, Wilson O.
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Best Local Similarity 100.0
Matches 22; Conservative
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ORGANISM: Homo Sapien
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Sequence 173. Application US/09328475C

Patent No. 6476207

GENERAL INFORMATION

APPLICANT: Astel, Jon H.

APPLICANT: Carroll III, Eddie

APPLICANT: Carroll III, Eddie

APPLICANT: Ford, Donna M.

APPLICANT: Ford, Donna M.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PROSTATE CANCER

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE

CURRENT APPLICATION NUMBER: US/09/328,475C

CURRENT APPLICATION NUMBER: US/09/328,475C

CURRENT APPLICATION OFTE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: FASESEQ for Windows Version 3.0

SEQ ID NO 73

LENGTH: 1024

TYPE: DNA

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.

APPLICANT: Astel, Jon H.

APPLICANT: Bridge, Wilson O.

APPLICANT: Endege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.

APPLICANT: Steinmann, Kathleen E.

APPLICANT: Steinmann, Kathleen E.

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICANTON UNDER: US/09/328,475C
CURRENT PILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 75

LINGTH: 1024
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US-09-328-475C-75/c
; Sequence 75, Application US/09328475C
; Patent No. 6476207
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i_CCATION: (1)...(1024)
i_CTHER INFORMATION: n = A,T,C or G
US-09-328-475C-73
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// LOCATION: (1)...(1024)
// OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-75
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ORGANISM: Homo Sapien
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Sequence 249, Application US/09188930A
; Sequence 249, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
    APPLICANT: Strachan, Lorna
    APPLICANT: Strachan, Lorna
    APPLICANT: Strachan, Matthew
    APPLICANT: Murison, James Greg
    TITLE OF INVENTION: Compositions Isolated From Skin Cells
    TITLE OF INVENTION: and Methods For Their Use
    TITLE REPERENCE: 11000.1011c1
    CURRENT APPLICATION NUMBER: US/09/188,930A
    CURRENT FILING DATE: 1998-11-09
    NUMBER: OF SEQ ID NOS: 348
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 249
    LENGTH: 1212
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Patent No. 6573095

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Streeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Murison Skin Cells
TITLE REFERENCE: 11000, 1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT APPLICATION NUMBER: US/09/312,283C
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 249
LENGTH: 1212
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100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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                                                                                                                                                     Query Match 1.3%; Score 22; DB 3; Length 1024; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 22; Conservative 0; Mismatches 0; Indels
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: [1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-86
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Best Local Similarity 100.
Matches 22; Conservative
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Best Local Similarity
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US-09-188-930-249
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-188-930-249/c
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Sequence 86, Application US/09328475C

Sequence 86, Application US/09328475C

Patent No. 6476207

GENERAL INFORMATION:

APPLICANT: Astel, Jon H.

APPLICANT: Endeg, Wilson O.

APPLICANT: Findeg, Wilson O.

APPLICANT: Schlegel, Nobert

APPLICANT: Schlegel, Nobert

TILLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

TILLE REFERENCE: 1532.002/200130.463

CURRENT APPLICATION UNMBER: 1950-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 86

LENGTH: 1024
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.

APPLICANT: Astel, Jon H.

APPLICANT: Badege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert B.

TITLE OF INVENTION: GARE DIPPERBNITALLY REGULATED IN PROSTATE CANCER;
TITLE OF INVENTION: GARE DIPPERBNITALLY REGULATED IN PROSTATE CANCER;
TITLE OF PAPPLICANT: 1932.002/200130.463

CURRENT APPLICANT: 1999-06-09

NUMBER OF SEQ ID NOS: 341

SOFTWARE: FASESEQ for Windows Version 3.0
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                          1.3%; Score 22; DB 3; Length 1024;
100.0%; Pred. No. 1.9;
tive 0; Mismatches 0; Indels
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1.3%; Score 22; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches
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                                                                                                                                   1692 AGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                             110 AGTACCTCGGCCGCGACCACGC 89
                                                                                                                                                                                                                                                              RESULT 72
18-09-328-475C-82/c
Sequence 82, Application US/09328475C
Patent No. 6476207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 AGTACCTCGGCCGCGACCACGC 83
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                                                                             22; Conservative
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
                          Query Match
Best Local Similarity
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                                                                                Matches
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Sequence 319, Application US/09389681A
| Sequence 319, Application US/09389681A
| Patent No. 6518237
| GENURAL INFORMATION:
| APPLICANT: Viqui, Jiang
| APPLICANT: Mitcham, Jennifer L.
| TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
| TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
| TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
| TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
| TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
| TITLE OF INVENTION: 1999-09-02
| TITLE OF INVENTION: 463
| GURRENT FILING DATE: 1999-09-02
| NUMBER OF SEQ ID NOS: 463
| SEQ ID NO 319
| LENGTH: 241
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APPLICANT: Harlocker, Subarian I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SEQ ID NO 319
LENGTH: 241
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GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
LOCATION: (1)...(241)
OTHER INFORMATION: n = A,T,C or G
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US-09-389-681-319
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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US-09-389-681-319
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APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TITLE REPERENCE: 506612000120
TITLE OF INVENTION NUMBER: US,10/10131,827
CURRENT APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TILE REPERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-06-08
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  0; Indels
  0; Mismatches
                                                       1692 AGTACCTCGGCCGCGACCACGC 1713
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US-10-131-827-8652
Sequence 8652, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
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Patent No. 6905827
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 100.0
Matches 21; Conservative
  22; Conservative
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US-10-131-827-8632
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US-10-131-827-8632
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SEQ ID NO 8632
LENGTH: 240
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Matches
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1693 GTACCTCGGCCGCGACCACGC 1713

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Sequence 319, Application US/09834759

Sequence 319, Application US/09834759

Patent No. 6680197

GENERAL INFORMATION:

APPLICANT Uliang, Vuqiu

APPLICANT: Dilang, Vuqiu

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Hepler, William T.

TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

TITLE OF INVENTION: UNDER: 200121.470C9

CURRENT APPLICATION UNDER: 2001-04-13

NUMBER OF SEQ ID NOS: 547

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 319
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Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels
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APPLICANT: Yugui, Jiang
APPLICANT: Yugui, Jiang
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.47006
CURRENT FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 479
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 319
LINGTH: 241
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APPLICANT: Yuqui, Jiang
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  208 GTACCTCGGCCGCGACCACGC 228
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CTHER INFORMATION: n = A,T,C or G
US-09-590-751A-319
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NAME/KEY: misc feature
LOCATION: (1)...(241)
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NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                          RESULT 82
US-09-834-759-319
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APPLICANT: Dilon, Davin C.
APPLICANT: Dilon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Witcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Ku, Jiangchun
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121.470C4
CURRENT APPLICATION NUMBER: US/09/433,826B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 474
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 319
LENGTH: 241
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Sequence 319, Application US/09604287A

GENERAL INFORMATION:
APPLICANT: Jang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William L.
APPLICANT: Hepler, William L.
APPLICANT: Hepler, William L.
APPLICANT: APPLICANT: COMPOSITIONS OF BREAST CANCER
TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER
FILE REPREADER: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
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100.0%; Pred. No. 5.7;
tive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 319
LENGTH: 241
                                                                                                                Sequence 319, Application US/09433826B
Patent No. 6579973
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqui
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208 GTACCTCGGCCGCGACCACGC 228
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NAME/KEY: misc_feature
LOCATION: (1)...(241)
OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-604-287A-319
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Matches 21; Conservative
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US-09-604-287A-319
                                                                                                  US-09-433-826B-319
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GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C11
CURRENT APPLICATION NUMBER: US/10/076,622
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 627
SOFTWARE: PaetSEQ for Windows Version 4.0
SEQ ID NO 319
LENGTH: 241
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APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FRSESEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 301
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100.0%; Pred. No. 5.7;
tive 0; Mismatches 0; Indels
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                                                                                 RESULT 86
US-10-076-622-319
; Sequence 319, Application US/10076622
; Patent No. 6958361
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
          208 GTACCTCGGCCGCGACCACGC 228
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Patent No. 6329505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc feature
LOCATION: 24, \overline{3}6, 39
OTHER INFORMATION: n = A,T,C or G
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Reed, Steven G.
Kalos, Michael
Fanger, Gary
Retter, Mark
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Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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) ORGANISM: Homo sapien
US-09-439-313-293
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APPLICANT:
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                                                                                                                                         ## APPLICANT: Yuqui, Jiang
### APPLICANT: Yuqui, Jiang
### APPLICANT: Dillon, Davin C.
### APPLICANT: Mitcham, Jennifer L.
### APPLICANT: Mitcham, Jennifer L.
### APPLICANT: Mitcham, Jennifer L.
### TITLE OF INVENTION: DIAGNOSITIONS FOR THE TREATMENT AND
### TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
### CURRENT APPLICATION NUMBER: US/09/551,621
### CURRENT FILING DATE: 2000-04-17
### NUMBER OF SEQ ID NOS: 479
### SOFTWARE: FastSEQ for Windows Version 3.0
### SEQ ID NO 319
### LENGTH: 241
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Sequence 319, Application US/09551621A

Sequence 319, Application US/09551621A

Sequence 319, Application US/09551621A

GENERAL INFORMATION:

APPLICANT: Value of Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: COMPOSITIONS FOR THE US/09/551,621A

TITLE OF INVENTION: US/09/551,621A

CURRENT APPLICATION NUMBER: 105/09/551,621A

CURRENT FILING DATE: 2000-04-17

NUMBER OF SEQ ID NOS: 479

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 319

LENGTH: 241
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208 GTACCTCGGCCGCGACCACGC 228
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i_CCATION: (1)...(241)
CTHER INFORMATION: n = A,T,C or G
US-09-551-621-319
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                                                                                                    RESULT 84
US-09-551-621-319
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CURRENT APPLICATION NUMBER: US/09/159,812A CURRENT FILING DATE: 1998-09-23 NUMBER OF SEQ ID NOS: 306 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 293 LENGTH: 301
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Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jannifer I.
APPLICANT: Mitcham, Jannifer I.
APPLICANT: Harlocker, Suean L.
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Patent No. 6620922
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Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Skeiky, Yasir A.W.
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Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
FILE REFERENCE: 210121.428C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stolk, John A.
                                                                                                                                    TYPE: DNA; ORGANISM: Homo sapien
US-09-159-812-293
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CORGANISM: Homo sapien
US-09-636-215-293
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APPLICANT:
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APPLICANT:
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APPLICANT:
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; Sequence 293, Application US/09232149A
; Sequence 293, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: W. Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchan, Jennifer Lynn
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; TITLE OF INVENTION: Lynn
; TITLE OF INVENTION: 120121.427C6
; CURRENT RPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
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APPLICANT: Xu, Jiangchun
APPLICANT: Xi, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
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100.0%; Pred. No. 5.7;
vative 0; Mismatches 0; Indels
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Patent No. 6613872
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Best Local Similarity 100.
Matches 21; Conservative
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ORGANISM: Homo sapien
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US-09-232-149A-293
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                                                          US-09-352-616A-293
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US-09-159-812-293
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LENGTH: 301
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION WHERE: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
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Query Match 1.2%; Score 21; DB 3; Length 301; Best Local Similarity 100.0%; Pred. No. 5.7; Matches 21; Conservative 0; Mismatches 0; Indels
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APPLICANT

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APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REPERENCE: 210121.427620

CURRENT APPLICATION NUMBER: US/09/679,426

CURRENT PILLING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 895

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 301
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CURRENT FILING DATE: 2001-01-12
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100.0%; Pred. No. 5.7;
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Best Local Similarity 100.0%; Pred. No. 5.7;
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SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6800746
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
  Susan L.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Matches 21; Conservative
                                                                                                                                  John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-293
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; ORGANISM: Homo sapien
US-09-759-143-293
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US-09-759-143-293
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42721
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 301
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dalllon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427D2
CURRENT APPLICATION NUMBER: 18/09/688,489
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 301
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100.0%; Pred. No. 5.7;
tive 0; Mismatches 0; Indels
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US-09-688-489-293
'S Equence 293, Application US/09688489
'Patent No. 6664377
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Patent No. 6759515
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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                  Henderson, Robert A.
Kalos, Michael D.
                                                                                                    Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Best Local Similarity 100.
Matches 21; Conservative
                                                                Fanger, Gary R.
Retter, Marc W.
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Yuqui
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CORGANISM: Homo sapien
US-09-685-166A-293
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CRGANISM: Homo sapien
US-09-688-489-293
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Matches 21; Conserva
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US-09-679-426-293
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 21012.427C19
CURRENT APPLICATION NUMBER: US/09/657,279
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 877
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 301
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wandanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
AITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
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5.7;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 301
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CURRENT FILING DATE: 2001-12-10
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Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Particia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Patent No. 6943236
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                                                                                                                                                                                                                                                                                                                                                         232 GTACCTCGGCGCGACCACGC 252
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Kalos, Michael D.
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Best Local Similarity 100.0
Matches 21; Conservative
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Best Local Similarity 100.
Matches 21, Conservative
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COGANISM: Homo sapiens
US-10-012-896-293
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CORGANISM: Homo sapien
US-09-657-279-293
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APPLICANT: Hepler, William
TITLE OF INVENTION: CAMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SEQ TO ...
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     Mismatches
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; Sequence 293, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Vedvick, Thomas S.
Carter, Darrick
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Hepler, William
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Retter, Marc W.
Stolk, John A.
     21; Conservative
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; ORGANISM: Homo sapien
US-09-651-236-293
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LENGTH: 301
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     Matches
                                                                                                                                 RESULT 96
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Squence 846, Application US/10131827

Squence 846, Application US/10131827

GENERAL INFORMATION:

APPLICANT: Wohlgemuth, Jay

APPLICANT: Wohlgemuth, Jay

APPLICANT: Wohlgemuth, Jay

APPLICANT: Pry, Kirk

APPLICANT: Pry, Kirk

APPLICANT: Pry, Wirk

APPLICANT: Ly, Ngoc

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUTE

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

TITLE OF INVENTION: USCO120

CURRENT APPLICATION NUMBER: US /10/131,827

CURRENT APPLICATION NUMBER: US 60/296,764

PRIOR PILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: US 60/296,764

PRIOR PILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 9090

SSQC ID NOS: 9090

SEQ ID NO 8546

LENGTH: 311
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Fatent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Ornust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 71
LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.2%; Score 21; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels
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1.2%; Score 21; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Homo sapiens
US-10-131-827-8546
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; ORGANISM: Human
US-09-188-930-71
RESULT 99
US-10-131-827-8546
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US-09-188-930-71/c
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Search completed: March 11, 2006, 23:05:09 Job time : 329 secs

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17771, A
100, Appl
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15, Appl
17222, A
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43996,
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US-09-814-353-11508
US-09-814-353-12779
US-09-814-353-12779
US-09-814-353-12869
US-10-198-846-7580
US-10-198-846-7580
US-10-198-846-7580
US-10-37-930-6566
US-09-814-353-18016
US-09-814-353-18016
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	Sequence 12584, A Sequence 17446, A Sequence 17448, Ap Sequence 165, App Sequence 15714, App Sequence 11012, A Sequence 11012, A Sequence 11012, A Sequence 1793, A Sequence 1124, Ap Sequence 1120, Ap Sequence 5599, Ap Sequence 1120, Ap Sequence 1120, Ap Sequence 11865, Ap Sequence 11865, Ap Sequence 11865, Ap Sequence 11885, Ap	Sequence 31, Appl Sequence (Appl 1) Sequence (1819, A Sequence 1181, Ap Sequence 11249, A Sequence 11249, A Sequence 114495, Sequence 11084, A Sequence 11084, A Sequence 11954, A Sequence 11978, A Sequence 310778, A Sequence 310778, A Sequence 310778, A Sequence 3117, Ap
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Db 1081 ATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1140	Oy 1141 TTCCAGGCACCGACACAGACTCGTCGGGGGCACCCTTGCTCCAGGTGTACTGCTAACCC 1200 1141 TTCCAGGCACCGACAGAGTCGGGGGGCACCCTTGCTCCAGGTGTACTCCTAACCC 1200	OY 1201 CTGCCAGGCCCACACCCTTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGG 1260 1201 CTGCCAGGCCCACCCACCCACCCCTTCTGGGAGAAGCATGGCCTACAGAATGAAGAGGG 1260	Oy 1261 GGACCAGGAACCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCCACTCTGGCTCCTCC 1320	Qy 1321 TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1380 1321 TGCCTTGGCTGACTGGGTTCCTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1380	Qy 1381 ICCTIGCATCCCGAGCTGGTCTGATCCCTGCCAGGGCCCCTTCCTT	Qy 1441 TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 1500 1441 TCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAACCCTG 1500	Qy 1501 ACTCCATCCCCTATTGCCACCTAACCAATCATGCAAACTTCTCCCTCC	OY 1561 TCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATT	Oy 1621 CTATGTTATGTTAGGAGTTGGTTCTTGGCTGATGTTCTGTATCTTAACATGAC 1680	Oy 1681 CACASTIGTAAGTACCICGGCACCACGC 1713 	RESULT 2 US-10-104-047-799 ; Sequence 799, Application US/10104047	; GENERAL INCRMATION: NO. USZU03023639ZAI ; APPLICANT: HELIX RESEARCH INSTITUTE ; TITLE OF INVENTION: NO. USZ003023639ZAIel full length cDNA	; CURRENT APPLICATION UNMBER: US/10/104,047 ; CURRENT FILING DATE: 2002-03-25 ; PRIOR APPLICATION NUMBER:	; PKIOK FILING DATE: ; NUMBER OF SEQ ID NOS: 4096 ; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 799	, LENGTH: 1785 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-104-047-799	Query Match 93.1%; Score 1594; DB 6; Length 1785; Best Local Similarity 99.9%; Pred. No. 0; Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Qy 1 ATGCCCGCCCTGGACACCCCGCCCAGCATCTGGGCTCCACGCTTGGGACGTGGGAG 60	Qy 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC 120
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                                      APPLICANT: Recina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
ITLE OF INVENTION: Compositions and Methods Rel
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT PILING DATE: 2001-11-21
PRIOR PILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin Version 3.1
SEQ ID NO 117
                                                                                                                                                                                                                                                                                                               Score 983; DB Pred. No. 0; Mismatches
Sequence 117, Application US/09989920
Patent No. US20020172957A1
GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 1103; Conservative
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US-09-989-920-117
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RESULT 4 US-09-989-920-117 ω

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APPLICANT: Macine, Roberto
APPLICANT: Macine, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Pluta, Jason
APPLICANT: Pluta, Jason
APPLICANT: Liu, Chenghua
APPLICANT: Div, Chenghua
APPLICANTON: Compositions and Methods Relating to Breast Specific Genes and Procurent APPLICATION NUMBER: US/09/989,890
CURRENT APPLICATION NUMBER: US/09/989,890
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
SEQ ID NO 104
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1430 GCTCATGGTCTTCAGGTGGCCTGATCATGGAAGTAAGGAGTTAGGCATTACCTTCTGGG 1489
                                                                               1490 AGTGAACCCTGACTCCCATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTC 1549
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                                                                                                    301 AGTGAACCCTGACTCCATCCCCCTATTGCCACCCTAACCAATCATGCAAACTTCTCCCTC 360
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                                                                                                                                                              1550 CCTGGGGTAATTCAACAGTTAAAAG 1574
                                                                                                                                                                                    361 CCTGGGGTAATTCAACAGTTAAAAG 385
                                                                                                                                                                                                                                                                                                          Sequence 104, Application US/09989890
; Publication No. US20040166105A1
; GENERAL INFORMATION:
APPLICANT: Salceda, Susana
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CORGANISM: Homo sapien
US-09-989-890-104
                                                                                                                                                                                                                                                                   RESULT 6
US-09-989-890-104
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APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERRNCE: DEX-0291
CURRENT PPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
SEQ ID NO S5
SEQ ID NO S5
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                                                                                                    1437 GTCTTCAGGTGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAAC 1496
                                                                                                                                                                                      GICTICAGGIGGCCTGATCATGGAAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAAC 1760
                                                                                                                                                                                                                                                1557 TAATTCAACAGTTAAAAGAAGCTTATCTTAAATGTATTGTATTGGGGGGGTGGGCAGGGCC 1616
                                                                                                                                                                                                                                                                                                                                                       CACTCTATGTTATGTTAAGGAGTTGGTTCTGGTTCTTGGCTGATGTTCTGTATCTTAACA 1676
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Patent No. US20020172957A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
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US-09-989-920-55
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US-09-989-920-55
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985 GCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTG 1044
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                                                       PRIOR FLILING DATE: 1997-12-23
PRIOR PELING DATE: 1997-12-23
PRIOR PELING DATE: 1997-12-23
PRIOR PLILING DATE: 1997-10-23
PRIOR PLILING DATE: 1998-04-03
PRIOR PLLING DATE: 1998-04-03
PRIOR PLLING DATE: 1998-10-21
PRIOR PLILING DATE: 1999-10-21
PRIOR PLILING DATE: 1999-10-24
PRIOR PLILING DATE: 1999-01-28
PRIOR PLLING DATE: 1999-02-24
PRIOR PLLING DATE: 1999-02-24
PRIOR PLLING DATE: 1999-03-31
PRIOR PLLING DATE: 1998-03-31
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GENERAL INFORMATION:
TITLE OF INVENTON:
CURRENT APPLICATION:
FILE REFERENCE: 2300-21302
CURRENT APPLICATION IN CANCEROUS CELLS AND THEIR METHODS OF USE II
CURRENT APPLICATION NUMBER: US/10/779,543
CURRENT APPLICATION NUMBER: 10/076,555
PRIOR PILING DATE: 2002-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1105 GGAGCTCCAGGGTACCCAGCAAGCCATGACTCAT 1138
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US-10-779-543-10096
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LOCATION: 355
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Sequence 123, Application US/10074475

Publication No. US200300928981

SERNEAL INFORMATION:

APPLICANT: Macina, Roberto

APPLICANT: Macina, Roberto

APPLICANT: Reria, Kalpana

APPLICANT: Karra, Kalpana

APPLICANT: Karra, Kalpana

APPLICANT: Cafferkey, Robert

APPLICANT: Cafferkey, Robert

APPLICANT: Liu, Chenghing

APPLICANT: Liu, Chenghing

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific

TITLE OF INVENTION: Genes and Proteins

FILE REPERENCE: DEX-0313

CURRENT APPLICATION NUMBER: 2002-02-13

CURRENT FILING DATE: 2002-02-13

PRIOR APPLICATION NUMBER: 60/268,292

PRIOR APPLICATION NUMBER: 60/268,292

MINDER OFF THE NUMBER: 60/268,292

MINDER OFF THE NUMBER: CONT. CONT.
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US-10-779-543-10096
US-10-779-543-10096
Squence 10096, Application US/10779543
Publication No. US2005027917A1
GENERAL INFORMATION:
APPLICANT: Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302
CURRENT APPLICATION: NUMBER: 104/0779,543
CURRENT PILING DATE: 2004-02-12
PRIOR PILING DATE: 2002-02-15
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SOFTWARE: Patentin version 3.1
SEQ ID NO 123
LENGTH: 386
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ORGANISM: Homo sapien
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1065 GACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGC 1124
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                                                         PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/068,755
PRIOR PILING DATE: 1997-12-23
PRIOR FILING DATE: 1990-16-24
PRIOR FILING DATE: 1990-04-03
PRIOR FILING DATE: 1990-04-03
PRIOR PILING DATE: 1990-10-21
PRIOR PILING DATE: 1990-10-21
PRIOR PILING DATE: 1990-01-04
PRIOR PILING DATE: 1990-01-28
PRIOR PILING DATE: 1990-01-31
PRIOR PILING DATE: 1990-02-31
PRIOR PILING DATE: 1990-03-31
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100.0%; Pred. No. 6.1e-149;
tive 0; Mismatches 0; Indels
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Innis, Michael A.
Garcia, Pablo Dominiquez
Sudduth-Klinger, Julie
Reinhard, Christoph
Giese, Klause
Randazzo, Filippo
Kennedy, Giulia C.
Pot, David
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US-10-076-555-34
; Sequence 34, Application US/10076555
; Publication No. US20030065156A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
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Dickson, Mark
Drmanac, Snezana
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Lamson, George
Drmanac, Radoje
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Best Local Similarity 100.0
Matches 300; Conservative
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ORGANISM: Homo sapiens
US-10-779-543-1705
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PRIOR APPLICATION NUMBER: 09/217,471
PRIOR PILING DATE: 1998-12-21
PRIOR PILING DATE: 1998-12-21
PRIOR PILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR PILING DATE: 1998-04-03
PRIOR PILING DATE: 1998-04-03
PRIOR PILING DATE: 1998-10-21
PRIOR PLING DATE: 2000-04-10
PRIOR PILING DATE: 2000-04-10
PRIOR PILING DATE: 2000-04-10
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1998-01-28
PRIOR PILING DATE: 1998-01-28
PRIOR PILING DATE: 1998-01-28
PRIOR PILING DATE: 1998-01-28
PRIOR PILING DATE: 1998-01-24
PRIOR PILING DATE: 1998-01-34
PRIOR PILING DATE: 1998-01-34
PRIOR PILING DATE: 1998-01-34
PRIOR PILING DATE: 1998-01-34
PRIOR PILING DATE: 1998-03-31
REMAINING PAIOR APPLICATION NUMBER: 60/075,954
PRIOR PILING DATE: 1998-03-31
REMAINING PAIOR APPLICATION NUMBER: 60/080,114
PRIOR PILING DATE: 1998-03-31
REMAINING PAIOR APPLICATION NUMBER: 60/080,114
PRIOR PILING DATE: 1998-03-31
REMAINING PAIOR APPLICATION NUMBER: 60/080,114
PRIOR PILING DATE: 1998-03-31
REMAINING PAIOR APPLICATION NUMBER: 60/080,114
PRIOR PILING DATE: 1998-03-31
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PRIOR PILING DATE: 1998-03-31
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REMAINING PAIOR APPLICATION NUMBER: 60/080,114
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Publication No. US20050227917A1
GENERAL INFORMATION:
APPLICANT: Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-2130.
CURRENT FILING DATE: 2004-02-12
PRIOR FILING DATE: 2002-02-15
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OTHER INFORMATION: n = A,T,C or G
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US-10-779-543-1705
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Query Match 14.5%; Score 249; DB 9; Best Local Similarity 99.7%; Pred. No. 1e-121; Matches 299; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapien
US-10-074-475-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-779-543-34
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; Publication No. US20050227917A1
; GENERAL INFORMATION:
    APPLICANT: Williams et al
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REPRENCE: 2300-21302
; CURRENT APPLICATION NUMBER: 10/7079,543
; CURRENT PILING DATE: 2004-02-12
; PRIOR FILING DATE: 2002-02-15
; PRIOR PILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-23
; PRIOR FILING DATE: 1998-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              800 TGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGCAGGACTACC
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APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Novel Human Genes and Gene Expression
TITLE OF INVENTION: Products I
FILE REPERENCE: 2300-1480
CURRENT PILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: BARLIER PELLIAN DATE: 1998-12-21
PRIOR PILING DATE: EARLIER FILING DATE: 1998-12-21
PRIOR PILING DATE: EARLIER FILING DATE: 1997-12-23
PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-21
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-21
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,234
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-27
NUMBER OF SEQ ID NOS: 844
SOFTWARE: PASESEQ for Windows Version 4.0
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Pred. No. 1e-121;
0; Mismatches 1; Indels
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Best Local Similarity 99.7
Matches 299; Conservative
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US-10-076-555-34
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Sequence 124, Application US/10074475

Sequence 124, Application US/10074475

Publication No. US20030092898A1

GENERAL INFORMATION:

APPLICANT: Salceda, Susana

APPLICANT: Macina, Roberto

APPLICANT: Recipon, Herve

APPLICANT: Karra, Kalpana

APPLICANT: Luu, Yongming

APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific

TITLE OF INVENTION: Compositions and Proteins

TITLE REPRESENCE: DEX-0313

CURRENT FILING DATE: 2002-02-13

CURRENT FILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 295

SOFTWARE: PatentIn version 3.1

SEQ ID NO 124

LENGTH: 654
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PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR PELICATION NUMBER: 09/297,648
PRIOR PELICATION NUMBER: PCT/US99/01619
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1998-01-28
PRIOR FILING DATE: 1998-02-24
PRIOR PILING DATE: 1998-02-24
PRIOR PELICATION NUMBER: 60/075,954
PRIOR APPLICATION NUMBER: 60/005,114
PRIOR PILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
Remaining Prior Application data removed - See File Wrapper or PALM.
SCROID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LUNGTH: 300
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Sequence 669570, Application US/11036317

Sequence 669570, Application US/11036317

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOUTHWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 669570
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PRIOR FILING DATE: 1997-12-23
PRIOR PELICATION NUMBER: 60/068,755
PRIOR PELICATION NUMBER: 60/080,664
PRIOR PELICATION NUMBER: 60/105,234
PRIOR PELICATION NUMBER: 60/105,234
PRIOR PELING DATE: 1998-10-21
PRIOR PELING DATE: 1998-10-21
PRIOR PELING DATE: 1998-10-21
PRIOR PELING DATE: 1999-01-28
PRIOR PELING DATE: 1998-01-28
PRIOR PELING DATE: 1998-03-31
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
FOCATION: 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 20, 10CATION: 2, 23, 24, 25, 28, 29, 30, 36, 41, 85, 89, 97, 106, 108, 10CATION: 115, 134, 139, 177, 185, 207, 232, 275, 283, 303, 320, 327, 10CATION: 356, 414, 451, 469, 551, 566, 582, 588, 591, 605, 631, 656, OTHER INFORMATION: n = A,T,C or G FEATURE:
NAME/KEY: misc_feature
: LOCATION: 661, 678, 681, 687, 689, 702, 706, 710, 711, 713, 722
US-10-779-543-5731
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US-11-036-317-669570
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Facent No. US20020172957A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Recipon, Herve

APPLICANT: Chen, Sei-Yu

APPLICANT: Chen, Sei-Yu

APPLICANT: Liu, Chenghuin

TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot

FILE REFERENCE: DEX. Vongeming

APPLICANT: Liu, Chenghuin

TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot

CURRENT FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-22

NUMBER OF SEQ ID NOS: 284

SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                  89 ATGATAAACCACCTCAGCCCCACCAAGCCGCCGCACCGGTAGACCAGAACCCCAAGGACC 148
                                                                                                                                                                                                                                                                                                                  149 CTGGCCACCATGGGCCAGAGAGCATTACCTTCATCTCTGGCTCTGCTGAGCCGGCCCTTG 208
                                                                                                                                                                                                                                                                                                                                                                                  61 CTGGCCACCATGGGCCAGAGAGCATTACCTTCATCTCTGGCTCTGCTGAGCCGGCCCTTG 120
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Publication No. US20050227917A1

GENERAL INFORMATION:

APPLICANT: Williams et al

TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

CURRENT APPLICATION NUMBER: US/10/779,543

CURRENT FILING DATE: 2004-02-12

PRIOR APPLICATION NUMBER: 10/076,555

PRIOR APPLICATION NUMBER: 09/217,471
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                      Length 654;
                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 TCTGCTTCCGCCGCTGCCGGGATTGCCTCCAGCGCTGTGGAG 310
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           Query Match 13.0%; Score 222; DB 5; Le Best Local Similarity 100.0%; Pred. No. 2.5e-107; Matches 222; Conservative 0; Mismatches 0;
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US-09-989-920-116/c
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US-10-779-543-5731
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LENGTH: 120
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Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: 1058716CATON OF THE REPRENCE: MRI-0078CN
TITLE OF INVENTION: 1058716CATON OF THE REPRENCE: MRI-0078CN
TITLE OF INVENTION: 1058716CN
TITLE OF INVENTION: 105871CN
TITLE OF INV
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APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOWEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: US-09-01-21
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PLING DATE: 2000-06-12
PRIOR PLING DATE: 2000-06-12
PRIOR PLING DATE: 2000-06-12
PRIOR PLING DATE: 2000-06-12
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-27
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1.5%; Score 25; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.041;
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Matches 25; Conservative 0; Mismatches
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; Publication No. US20030165831A1
; GENERAL INFORMATION:
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-37484
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ORGANISM: Homo sapiens
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US-10-357-930-7524/c
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Sequence 4473, Application US/20131827

Bublication No. U520040009479A1

GENERAL INFORMATION:

APPLICANT: Woodward, Robert

TITLE OF INVENTION: GHRONIC INFLAMMATORY DISEASES

FILE REPERENCE: So6612000120

CURRENT APPLICATION NUMBER: US/10/131,827

CURRENT APPLICATION NUMBER: US/006,290

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-06-08

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 9990

SOFTWARE: Patentin version 3.1
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Sequence 31484, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel. Robert

APPLICANT: Endege, Wilson

APPLICANT: Endege, Wilson

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE

CURRENT PILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR PILING DATE: 2000-02-17

PRIOR PLING DATE: 2000-03-16

PRIOR PLING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/2107,454

PRIOR PLING DATE: 2000-05-25

PRIOR PLING DATE: 2000-06-09

PRIOR PLING DATE: 2000-06-13

PRIOR PLING DATE: 2000-06-09

PRIOR PRIOR PLING DATE: 2000-06-09

PRIOR PRIOR DATE: 2000-06-09

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PRIOR PRIOR DATE: 2000
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     1 GATGTTAAGCTCAAAGGCATCCCTG 25
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LOCATION: (1)..(224)
OTHER INFORMATION: n = A, C, T or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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US-10-357-930-37484/c
                                                                                                                                                            RESULT 17
US-10-131-827-8473
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280 GTAAGTACCTCGGCCGCGACCACGC 304
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; ORGANISM: Homo sapiens
US-10-060-036-4393
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US-10-060-036-4393
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US-09-814-353-5095
i Sequence 5095, Application US/09814353
i Publication No. US20030165831A1
general Information:
APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR PRIOR FILING DATE: 2000-07-27
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Pred. No. 0.04;
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PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR PILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 123, 131, 149, 152, 166, 201, 284
OTHER INFORMATION: n = A,T,C or G
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US-09-814-353-5095
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SEQ ID NO 5095
LENGTH: 310
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RESULT 22
US-09-814-353-11387
is Sequence 11387, Application US/09814353
is Publication No. US20030165831A1
is GENERAL INFORMATION:
is APPLICANT: Lee, John
is APPLICANT: Lillie, James
it TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR ITILE OF INVENTION: HERAPY OF OVARIAN CANCER
it TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
it TILLIE OF INVENTION: USER: US 60/191,031
is PRIOR APPLICATION NUMBER: US 60/207,124
is PRIOR PELING DATE: 2000-05-25
is PRIOR PELING DATE: 2000-06-15
is PRIOR PELING DATE: 2000-06-15
is PRIOR FILLING DATE: 2000-06-15
is PRIOR FILLING DATE: 2000-07-07
is PRIOR FILLING DATE: 2000-07-07
is PRIOR FILLING DATE: 2000-07-25
is PRIOR FILLING DATE: 2000-07-27
is NUMBER OF SEQ ID NOS: 22037
is SOFTWARE: PRESERE OF WINDOWS VERSION 4.0
is SED ID NO 11387
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Publication No. US20030073144A1

GENERAL INFORMATION:

APPLICANT: Ralos, Michael D.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Hepler, William T.

APPLICANT: Jang, Yugiu

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF PANCREATIC CANCER

FILE REPERENCE: 210121.566

CURRENT PAPLICANTON: NUMBER: US/10/060,036

CURRENT PLING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4393
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100.0%; Pred. No. 0.039;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.04;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.4
Matches 25; Conservative
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US-10-198-846-5605/C
US-10-198-846-5605, Application US/10198846
; Sequence 5605, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Ku, Yongyao
APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: TRERAPY OF BREAST CANCER
; TILLE REPERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5605
; LENGTH: 1252
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| NAME/KEY: misc_feature
| LOCATION: 1126, 1128, 1137, 1138, 1140, 1141, 1144, 1148, 1151,
| LOCATION: 1156, 1165, 1166, 1173, 1176, 1183, 1188, 1193, 1194, 1195,
| LOCATION: 1199, 1201, 1209, 1212, 1215, 1216, 1220, 1221, 1222, 1223,
| LOCATION: 1224, 1230, 1231, 1239, 1240, 1243, 1244, 1245, 1252
| UCHER INPORMATION: n = A,T,C or G
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                                                                                 DB 6; Length 810; 0.038;
                                                                                                                                        0; Indels
                                                                              Query Match 1.5%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                            1689 GTAAGTACCTCGGCCGCGACCACGC 1713
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ORGANISM: Homo sapiens
FEATURE:
; ORGANISM: Homo sapien
US-10-074-511-10
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APPLICANT: Recipon, Herve
APPLICANT: Rarra, Kalpan
APPLICANT: Karra, Kalpan
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
FILE REFERENCE: DEX-0314
CURRENT APPLICATION NUMBER: US/10/074,511
CURRENT FILING DATE: 2001-02-12
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
SEQUENCE: PatentIn version 3.1
SEQUENCE: PatentIn version 3.1
TYPE: DNA
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                                                                                                                                                                                                        US-09-1844-353-11/71, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Libompson, Pamela

APPLICANT: Libompson, Pamela

APPLICANT: Libompson, Pamela

APPLICANT: Libompson, Pamela

TITLE OF INVENTION: UDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MRI-0068

CURRENT FILING DATE: 2001-03-21

CURRENT FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-25

PRIOR PRIOR FILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-25

PRIOR PRIOR FILING DATE: 2000-07-25

PRIOR PRIOR PRESENCE: 2000-07-25

PRIOR PRIOR DATE: 2000-07-25

PRIOR PRIOR PRIOR DATE: 2000-07-25
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1.5%; Score 25; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                          428 GTAAGTACCTCGGCCGCGACCACGC 452
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APPLICANT: Salceda, Susana; APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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US-10-074-511-10/c
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Publication No. US20030165831A1
GENERAL INFORMATION:
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US-10-47-45-15
Sequence 15, Application US/10477445
Sequence 15, Application WS/10477445
Sequence 15, Application WS/10477445
Sequence 15, Application WS/10477445
SEQUENCE INFORMATION:
TITLE OF INFORMATION:
TITLE OF INFORMATION:
FILE REPRENCE RCK-12
CURRENT APPLICATION WIMBER: US/10/477,445
CURRENT APPLICATION NUMBER: PCT/EP02/05127
FRIOR PEDICATION NUMBER: PCT/EP02/05127
FRIOR FILING DATE: 2002-05-10
FRIOR FILING DATE: 2001-05-11
SEQ ID NO 15
IRNGHE OF SEQ ID NOS: 111
SEQ ID NO 15
FRIOR FILING DATE: 2001-05-11
SEQ ID NO 15
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                                                             Sequence 1051, Application US/10950009
(BURDAL INFORMATION:
APPLICANT: BERKA, Randy
APPLICANT: BASHKIROVA, Elena
TITLE OF INVENTION: Methods
CURRENT APPLICATION: Methods
CURRENT APPLICATION NUMBER: US/10/950,009
CURRENT APPLICATION NUMBER: US/10/950,009
CURRENT APPLICATION NUMBER: 05/506,140
PRIOR PILICATION NUMBER: 60/506,140
PRIOR FILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1190
SOFTWARE: FBESTEQ for Windows Version 4.0
LENGTH: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 1.4%; Score 24; DB 9; Length 150; Similarity 100.0%; Pred. No. 0.14; 24; Conservative 0; Mismatches 0; Indels
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0.14;
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
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LOCATION: 145.7145
OTHER INFORMATION: unknown nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: 231..231
; CTER INORATION: unknown nucleotide
US-10-477-445-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-814-353-17222/c
; Sequence 17222, Application US/09814353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 TAAGTACCTCGGCCGCGACCACGC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                              US-10-950-009-1051/c
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Query Match
1.4%; Score 24; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-25
PRIOR PLLING DATE: 2000-07-25
PRIOR PLLING DATE: 2000-07-25
PRIOR PLLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 13395
                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-814-353-16395
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; ORGANISM: Homo sapiens
US-09-814-353-3678
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                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Publication No. US20030165831A1
Fubblication No. US20030165831A1
FITLE OF INVENTION: DEMTIFICATION, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MIS-068
CURRENT APPLICATION NUMBER: US 60/191,031
FRIOR PEDICATION NUMBER: US 60/191,031
FRIOR FILING DATE: 2000-05-25
FRIOR APPLICATION NUMBER: US 60/211,940
FRIOR APPLICATION NUMBER: US 60/211,940
FRIOR FILING DATE: 2000-06-15
FRIOR PEDICATION NUMBER: US 60/216,820
FRIOR PEDICATION NUMBER: US 60/216,820
FRIOR FILING DATE: 2000-07-07
FRIOR PEDICATION NUMBER: US 60/220,661
FRIOR FILING DATE: 2000-07-25
FRIOR FILING DATE: 2000-07-25
FRIOR FILING DATE: 2000-07-25
FRIOR PEDICATION NUMBER: US 60/257,672
FRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SECOTUMENT PARCES FARESED FOR WINDOWS VERSION 4.0
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; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; APPLICANT: Lillie, James
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-0068
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT APPLICATION NUMBER: US 60/191,031
; PRIOR PILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR PLICATION NUMBER: US 60/207,124
; PRIOR PLICATION NUMBER: US 60/211,940
; PRIOR PILING DATE: 2000-06-25
; PRIOR APPLICATION NUMBER: US 60/211,940
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                                 DB 3; Length 274; 0.14;
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1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches
                           Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 24; Conservative 0; Mismatches
                                                                                                                                                1690 TAAGTACCTCGGCCGCGACCACGC 1713
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US-09-814-353-11632/c
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LENGTH: 274
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APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lilia, James
AITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT FILIAGO ADTE: 2001-03-21
FRICA REPLICATION NUMBER: US 60/191,031
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLILING DATE: 2000-07-25
PRIOR PRILING DATE: 2000-07-25
PRIOR PRING PRI
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0.14;
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
                                                                                              1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3678, Application US/09814353 Publication No. US20030165831A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 9991, Application US/09814353; Publication No. US20030165831A1; GENERAL INFORMATION:
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US-US-104-23-53-629/0/, Application US/09814353
; Sequence 2976, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Inflie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPAIAN CANCER
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REPERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/201,124
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR PILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITIONS, KITS, AND METHODS FOR ASSESSMENT, PREVENTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 312; 0.14;
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                                                                                                                                                                                                    US-09-814-353-10381/C

US-09-814-353-10381/C

Sequence 10381, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lie-, John

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, NOVEL GENES, COMPOSITIONS, KIT

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MRI-006B

CURRENT APPLICATION NUMBER: US/09/814,353

CURRENT APPLICATION NUMBER: US 60/191,031

PRIOR PILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-
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                              1690 TAAGTACCTCGGCCGCGACCACGC 1713
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US-09-814-353-2976/c
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APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: US 60/211,940
PRIOR PLILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR PLILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
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               NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF OVARIAN CANCER
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1.4%; Score 24; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.14;
ive 0; Mismatches 0; Indels
           TITLE OF INVENTION: NOWEL GENES, COMPOSITION
TITLE OF INVENTION: IDENTIFICATION, ASSESSMI
TITLE OF INVENTION: IDENTIFICATION, ASSESSMI
TITLE OF INVENTION: THERAPY OF OVARIAN CANCIS
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/250,651
PRIOR PILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/250,672
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SEQ ID NOS: 22037
SEC ID NO 9991
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Lee, John
James
NOVEL GENES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 24; Conservative
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US-09-814-353-4074
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US-09-814-353-4074/c
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SEQ ID NO 4074
LENGTH: 312
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Publication No. US20040110668A1
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; Sequence 9305, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Lille, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: NOVEL GENES, COMPOSITION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: NUMBER: US 60/191,031
; PRIOR PILING DATE: 2000-03-21
; PRIOR PILING DATE: 2000-03-21
; PRIOR PILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-27
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-27
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1.4%; Score 24; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2976
LENGTH: 319
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                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

| LOCATION: 181, 183, 191, 314

| OTHER INFORMATION: n = A,T,C or G

US-09-814-353-2976
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LCCATION: 181, 183, 191, 314

CTHER INFORMATION: n = A,T,C or G

US-09-814-333-9305
                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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US-09-814-353-9305/c
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30 TAAGTACCTCGGCCGCGACCACGC 7

; Sequence 1870, Application US/09969034

RESULT 39 US-09-969-034-1870

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APPLICANT: Burgeas Christopher C.
APPLICANT: Aarlie John H.
APPLICANT: Aarlie John H.
APPLICANT: Aarlie John H.
APPLICANT: Aarlie John H.
APPLICANT: Cation, Theodore J.
APPLICANT: Molinoi Gary A.
APPLICANT: Molinoi Ga
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Sequence 11010, Application US/09814353
; Publication No. US20030165831A1
; Publication No. US20030165831A1
; Publication No. US20030165831A1
; Publication No. US20030165831A1
; APPLICANT: Hee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Liblie, James
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: IDENTIFICATION, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, AND STILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT APPLICATION NUMBER: US 60/191,031
; PRIOR PILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR PILING DATE: 2000-06-15
; PRIOR PILING DATE: 2000-07-07
; PRIOR PILING DATE: 2000-07-27
; PRIOR PILING DATE: 2000-07-27
; PRIOR PILING DATE: 2000-07-27
; PRIOR PILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE FEASTER OF WINDOWS VETSION 4.0
; SEQ ID NO 11010
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1.4%; Score 24; DB 3; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.4%; Score 24; DB 3; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 4711
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1 LCCATION: 204

2 OTHER INFORMATION: n = A,T,C or G

US-09-814-353-4711
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US-09-814-353-11010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-814-353-11010/c
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US-10-357-930-7995/c

Sequence 7995, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlagel. Robert

APPLICANT: Endege, Wilson

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND THERAPY OF

TITLE OF INVENTION: DEBNITFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: UNDERR. US/10/357,930

TITLE OF INVENTION: MUMBER: 09/788,276

FRIOR APPLICATION NUMBER: 09/788,276

PRIOR FILING DATE: 2000-02-16

PRIOR FILING DATE: 2000-02-16

PRIOR FILING DATE: 2000-02-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-01-18

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR APPLICATION NUMBER: 60/215,281

PRIOR PRILING DATE: 2000-01-18

PRIOR PRILING DATE: 2000-01-18
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| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lee, John
| APPLICANT: Thompson, Pamela
| APPLICANT: Lillie, James
| APPLICANT: Lillie, James
| TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
| TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
| TITLE OF INVENTION: INTERAPY OF OVARIAN CANCER
| FILE REPERENCE: MRI-0068
| CURRENT APPLICATION NUMBER: US/09/814,353
| CURRENT APPLICATION NUMBER: US/09/814,353
| PRIOR APPLICATION NUMBER: US 60/191,031
| PRIOR PILLING DATE: 2000-03-21
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0
                                                                                                        Length 326;
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1.4%; Score 24; DB 8; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                          0; Indels
                                                                                                        DB 3;
                                                                                                     Query Match

1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                             1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                                    113 TAAGTACCTCGGCGCGACCACGC 90
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OTHER INFORMATION: n = A, T, C or G
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US-10-357-930-7995
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             ; OTHER INFORMATION OF US-09-814-353-17947
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POSITIONS, KITS, AND METHODS FOR ASSESSMENT, PREVENTION, AND THERAPY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence (666, Application US/10357930
| Publication No. US20040259086A1
| GENERAL INPORMATION: | APPLICANT: Schegel. Robert | TITLE OF INVENTION: IDENTIFICATION ASSESSMENT, FITLE OF INVENTION: HUMAN PROSTATE CANCER | TITLE OF INVENTION: HUMAN PROSTATE CANCER | TITLE OF INVENTION: HUMAN PROSTATE CANCER | FILE REFERENCE: MRI-00760 | CURRENT FILING DATE: 2003-02-04 | PRIOR APPLICATION NUMBER: 60/183,319 | PRIOR FILING DATE: 2000-02-17 | PRIOR PRILING DATE: 2000-03-16 | PRIOR APPLICATION NUMBER: 60/189,862 | PRIOR PRILING DATE: 2000-03-16 | PRIOR PRILING DATE: 2000-03-16 | PRIOR PRILING DATE: 2000-05-25 | PRIOR APPLICATION NUMBER: 60/219,007 | PRIOR PRILING DATE: 2000-07-18 | PRIOR PRINK DATE STORE SEQ ID NOS: 62232 | SOFTWARE FEASESEQ FOR Windows Version 4.0 | SEQ ID NO 6066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 24; Conservative 0; Mismatches
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: PSESEQ for Windows Version 4.0
; SEQ ID NO 12238
; LENGTH: 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                     TYPE: DNA

GRGANISM: Homo sapiens
FRATURE:

NAME/KEY: misc_feature

LOCATION: 236, 252, 254, 313, 322, 329

COTHER INFORMATION: n = A,T,C or G

US-09-814-353-12238
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; ORGANISM: Homo sapiens
US-10-357-930-6066
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US-09-814-353-16765/c
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                                                                                                                                                                                       US-US-19-18-15-59-59 (Application US/09814353)

Publication No. US20030165831A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Libromeon, Pamela
APPLICANT: Libromeon, THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
CURRENT AILING DATE: 2000-03-21
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-00-07
PRIOR FILING DATE: 2000-00-07
PRIOR PILING DATE: 2000-00-07
PRIOR PILING DATE: 2000-00-07
PRIOR PILING DATE: 2000-00-07
PRIOR PILING DATE: 2000-01-12-11
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: Pastese for Windows Version 4.0
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UKS-09-614-353-12238/C
Sequence 12238, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lillie, Jamela
APPLICANT: Lillie, Jamela
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: US/09/814,353
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/21,124
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PLING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PLING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches
   1690 TAAGTACCTCGGCCGCGACCACGC 1713
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; LOCATION: 236, 252, 254, 313, 322, 329
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5958
                               30 TAAGTACCTCGGCCGCGACCACGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 TAAGTACCTCGGCCGCGACCACGC 7
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ORGANISM: Homo sapiens
                                                                                                                                                  RESULT 44
US-09-814-353-5958/c
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Publication No. US20030165831A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9231, Application US/09814353 Publication No. US20030165831A1 GENERAL INFORMATION:
APPLICANT: Lee, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA; ORGANISM: Homo sapiens
US-09-814-353-9231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 49
US-09-814-353-9231/c
        US-09-814-353-2902
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Matches
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US-09-814-153-2902/C

Sequence 2902, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Lillie, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: OF OVARIAN CANCER

TITLE OF INVENTION: OF OVARIAN CANCER

TITLE OF INVENTION: OF OO1-03-21

CURRENT APPLICATION NUMBER: US 60/191, 031

PRIOR PLILNG DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-22

PRIOR FILING DATE: 2000-07-22

PRIOR FILING DATE: 2000-07-22

PRIOR FILING DATE: 2000-07-22

PRIOR APPLICATION NUMBER: US 60/257,672

PRIOR FILING DATE: 2000-07-22

PRIOR APPLICATION NUMBER: US 60/257,672

PRIOR APPLICATION NUMBER: US 60/257,672
                                                                                                                                                                                    APPLICANT: Information Fauncia
APPLICANT: Infile, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-066B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-25
PRIOR PAPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PELING DATE: 2000-17-25
PRIOR PELING DATE: 2000-17-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PELING DATE: 2000-17-25
PRIOR PELING DATE: 2000-17-25
PRIOR PELING DATE: 2000-17-25
PRIOR PELING DATE: 2000-17-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PELING DATE: 2000-17-25
PRIOR PELING DATE: 2000-17-25
PRIOR PELING DATE: 2000-17-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PELING DATE: 2000-17-25
PRIOR PELING DATE: 200
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1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches
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Sequence 16765, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 raagraccredecedeceded 78
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ORGANISM: Homo sapiens
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APPLICANT: Lee, James
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT PELLING DATE: 2001-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PLLING DATE: 2000-03-21
PRIOR PLLING DATE: 2000-05-25
PRIOR PLLING DATE: 2000-06-15
PRIOR PLLING DATE: 2000-06-15
PRIOR PLLING DATE: 2000-06-15
PRIOR PLLING DATE: 2000-07-07
PRIOR PLLING DATE: 2000-07-07
PRIOR PLLING DATE: 2000-07-22
PRIOR PLLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARRE: FastLERQ for Windows Version 4.0
SEQ ID NO 9211
LENGTH: 391
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APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, James
APPLICANT: Thompson, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-06B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US/0191,031
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: US/09/00-05-25
PRIOR FILING DATE: US/09/00-05-25
PRIOR PLING DATE: US/09/00-05-25
PRIOR PLING DATE: US/09/00-05-25
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
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US-09-814-353-3267/c

i Sequence 3267, Application US/09814353

i Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Lee, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILLS REFERENCE: MRI-006B

CURRENT APPLICATION NUMBER: US 60/191,031

PRIOR FILLING DATE: 2000-03-21

PRIOR FILLING DATE: 2000-05-25

PRIOR PELICATION NUMBER: US 60/211,940

PRIOR FILLING DATE: 2000-06-25

PRIOR PELICATION NUMBER: US 60/216,820

PRIOR FILLING DATE: 2000-07-25

PRIOR PELICATION NUMBER: US 60/257,672

PRIOR FILLING DATE: 2000-07-25

PRIOR PRIOR FILLING DATE: 2000-07-27

PRIOR PRIOR FILLING DATE:
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1.4%; Score 24; DB 3; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION WUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PILING DATE: 2000-12-21
NUMBER: OF SEQ ID NOS: 22037
SEQ ID NO 16375
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| LOCATION: 327, 378, 384

| CTHER INFORMATION: n = A,T,C or G

US-09-814-353-3267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-814-353-16375
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ORGANISM: Homo sapiens
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RESULT 52 US-09-814-353-9592/c

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| Sequence 8:92, Application Us/09814331
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POSITIONS, KITS, AND METHODS FOR ASSESSMENT, PREVENTION, AND
   IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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US-09-814-353-5221/C

US-09-814-353-5221/C

Sequence 5221, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thilis, James

ITILE OF INVENTION: THERAPY OF OVARIAN CANCER

ITILE OF INVENTION: THERAPY OF OVARIAN CANCER

ITILE APPLICATION NUMBER: US/09/814,353

CURRENT FILING DATE: 2001-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: US 60/191,031

PRIOR PILING DATE: 2000-03-25

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-25

PRIOR PILIN
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                                       THERAPY OF OVARIAN CANCER
                                                           TILE REPERRICE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/201,940
PRIOR PILING DATE: 2000-05-15
PRIOR PILING DATE: 2000-05-15
PRIOR PILING DATE: 2000-07-07
PRIOR PRILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEC ID NOS: 22037
SEC ID NO 17159
LENGTH: 415
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LOCATION: 271
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US-09-814-353-17159
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APPLICANT: Inilise, James
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS POR
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
ITILE OF INVENTION: THERAPY OF OVARIAN CANCER
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR PLILING DATE: 2001-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-22
PRIOR PLILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-07-07
PRIOR PLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-27
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lie, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 404;
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1.4%; Score 24; DB 8;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches (
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Matches 24; Conservative 0; Mismatches
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8043
LENGTH: 404
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
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                                                                                                                                                                                                                                                                    | NAME/KEY: misc_feature
| LCCATION: 37, 54, 147
| CTHER INFORMATION: n = A,T,C or G
| US-10-357-930-8043
                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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US-09-814-353-17159/c
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SEQUENCE 15689, APPLICATION US/09H14353

SEQUENCE 15689, APPLICATION US/09H14353

GENERAL INFORMATION:

APPLICANT: Led, John
APPLICANT: Lillie, James

TITLE OF INVENTION: NOWEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

PRICE REPRESENCE: MIL-OOGEB

CURRENT FILING DATE: 2001-03-21

PRICE PLING DATE: 2000-03-21

PRICE PLING DATE: 2000-03-21

PRICE PLING DATE: 2000-05-25

PRICE PLING DATE: 2000-07-07

PRICE PLING DATE: 2000-07-25

PRICE PLING DATE: 2000-07-27

PRICE PLING DATE: 2000-07-25

PRICE PLING DATE: 2000-07-27

PRICE PLING DATE: 2000-07-27

PRICE PLING DATE: 2000-07-25

PRICE PLING DATE: 2000-07-27

PRICE PLING DATE: 2000-07-27
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100.0%; Pred. No. 0.13;
tive 0; Mismatches
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR PRILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PastSEQ for Windows Version 4.0
SSOFTWARE: 420
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Best Local Similarity 100.0
Matches 24; Conservative
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US-09-814-353-12779
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US-09-814-353-5813
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                                                                                                                                                                                                                                                                                                                          Sequence 11508, Application US/09814353
| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Let, John
| APPLICANT: Lillib. James
| APPLICANT: Lillib. James
| APPLICANT: Lillib. James
| TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
| TITLE OF INVENTION: UDENTIFICATION, AND
| TITLE OF INVENTION: UDENTIFICATION, AND
| TITLE OF INVENTION: UNMER: US 60/191,031
| PRIOR FILING DATE: 2000-03-21
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-07-25
| PRIOR FILING DATE: 2000-12-21
| WUMBER OF SEQ ID NOS: 22037
| SEQ ID NO 11508
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; Sequence 12779, Application No. US20030165831A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFRENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US 60/191,031
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-03-21
; PRIOR PILING DATE: 2000-03-21
                                         Gaps
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100.0%; Pred. No. 0.13;
ive 0; Mismatches 0; Indels
                                         0; Indels
Best Local Similarity 100.0%; Pred. No. 0.13; Matches 24; Conservative 0; Mismatches
                                                                                                     1690 TAAGTACCTCGGCCGCGACCACGC 1713
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US-09-814-353-11508
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Best Local Similarity 100.0
Matches 24; Conservative
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LOCATION: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                            US-09-814-353-11508/c
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US-09-814-353-12779
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RESULT 63
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Sequence 39249, ApDication US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Endege, Wilson

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSIATE CANCER

FILE REPRENENCE: MRI-OOPBR.

CURRENT APPLICATION NUMBER: 09/785,276

PRIOR PELING DATE: 2003-02-04

PRIOR PELING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR PILING DATE: 2000-03-16

PRIOR PILING DATE: 2000-03-16

PRIOR PELING DATE: 2000-03-16

PRIOR PELING DATE: 2000-06-09

PRIOR PILING DATE: 2000-06-09

PRIOR PELING DATE: 2000-06-09

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-02-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18
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APPLICANT: Incompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPRESENCE: MIL-066B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR PLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-05-25
PRIOR PLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-05-25
PRIOR PLICATION NUMBER: US 60/211,940
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLICATION NUMBER: US 60/220,661
PRIOR PLICATION NUMBER: US 60/220,661
PRIOR PLICATION NUMBER: US 60/257,672
PRIOR PLICATION DATE: 2000-07-25
PRIOR PLICATION NUMBER: US 60/257,672
PRIOR PLICATION DATE: 2000-07-25
PRIOR PLICATION NUMBER: US 60/257,672
PRIOR PLICATION SATE: 2000-07-25
PRIOR PLICATION SATE: 2000-07-25
PRIOR PLICATION NUMBER: US 60/257,672
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 39249
LENCTH: 424
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US-09-814-353-5813
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US-10-357-930-39249/c
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; ORGANISM: Homo :
US-10-357-930-39249
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; Sequence 7580, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Ku, Yongyao
; APPLICANT: Ku, Yongyao
; APPLICANT: Steinmann, Kathleen
; APPLICANT: Steinmann, Kathleen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: FOR IDENTFICATION, ASSESSMENT, PREVENTION,
; TITLE OF INVENTION: FOR IDENTFICATION, ASSESSMENT, PREVENTION,
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REPERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT APPLICATION NUMBER: 60/306,220
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR APPLICATION NUMBER: 60/306,220
; RROR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7580
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UK-09-611-0-3
UK-09-61-0-3
UK-
                                                                                            Gaps
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    DB 8; Length 424;
0.13;
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                                                                                            0; Indels
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1.4%; Score 24; DB 5;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
Query Match
1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                               1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                  85 raagraccregecegeeaceacee 62
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LCCATION: 384
COTHER INFORMATION: n = A,T,C or G
US-10-198-846-7580
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US-10-198-846-7580/c
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THERAPY OF OVARIAN CANCER
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Sequence 6566, Application US/10357930

Sequence 6566, Application US/20040259086A1

SEGNERAL INRORANTION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: INDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: UNMER: US/10/357,930

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-16

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-06-25

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR PRIOR APPLICATION NUMBER: 60/211,314

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-07-18

PRIOR PILING DATE: 2000-07-18

PRIOR PILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 6223-

NUMBER OF SEC ID NOS: 6223-

SETURATED FOR SECTION NUMBER: 60/255,281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                  Query Match
1.4%; Score 24; DB 3; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18496
LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                               1690 TAAGTACCTCGGCCGCGACCACGC 1713
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICAT: Lee, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 TAAGTACCTCGGCCGCGACCACGC 7
                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-18496
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Best Local Similarity
Matches 24; Conserva
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US-09-814-353-18622/c
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GREEKAL INCHARATION:
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE
CURRENT APPLICATION NUMBER: 09/185,276
PRIOR PELING DATE: 2003-02-16
PRIOR PELING DATE: 2000-02-17
PRIOR PELING DATE: 2000-02-17
PRIOR PELING DATE: 2000-02-17
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-29
PRIOR PELING DATE: 2000-07-18
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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PSESEE FOR WINDOWS VERSION 4.0
SEQ ID NO 18622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1690 TAAGTACCTCGGCCGCGACCACGC 1713
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; ORGANISM: Homo sapiens
US-09-814-353-18622
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ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1690 TAAGTACCTCGGCCGCGACCACGC 1713
                                                                                                                                                                                                                                                                                                                                       FEATURE:
| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: 182, 223, 225, 281, 285, 392
| OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9426
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8.09-814-353-15845/c
; Sequence 15845, Application US/09814353
; Publication No. US20030165831A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 TAAGTACCTCGGCCGCGACCACGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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US-09-814-353-18016/c
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                                                                                                                                                                                                  Sequence 3100, Application US/09814353

Publication No. US20030165831A1

Sequence 3100, Application US/09814353

Publication No. US20030165831A1

SERBERAL INFORMATION:

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Allis, Jame

APPLICANT: Allis, Jame

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: IDENTIFICATION, AND

FILE REFERENCE: MRI-0668

CURRENT APPLICATION NUMBER: US/09/814,353

CURRENT APPLICATION NUMBER: US 60/191,031

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-22

PRIOR FILING DATE: 2000-07-22
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Sequence 9426, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: UNMBER: US 00/19/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/201,124
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/201,124
PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15
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. 0.13;
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
   1690 TAAGTACCTCGGCCGCGACCACGC 1713
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; LOCATION: 182, 223, 225, 281, 285, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-3100
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ORGANISM: Homo sapiens
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; Sequence 18016, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Lee, John
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REPRENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/201,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR PILING DATE: 2000-06-15
; PRIOR PILING DATE: 2000-06-15
; PRIOR PILING DATE: 2000-07-25
; PRIOR PILING DATE: 2000-07-25
; PRIOR PILING DATE: 2000-07-25
; PRIOR PILING DATE: 2000-07-27
; PRIOR PILING DATE: 2000-07-25
; PRIOR PILING DATE: 2000-07-27
; PRIOR PILING DATE: 2000-07-27
; PRIOR PILING DATE: 2000-07-25
; PRIOR PILING DATE: 2000-07-25
; PRIOR PILING DATE: 2000-07-27
; PRIOR PILING DATE: 2000-07-25
; PRIOR PILING DATE: 2000-07-27
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1.4%; Score 24; DB 3; Length 437;
100.0%; Pred. No. 0.13;
tive 0; Mismatches 0; Indels
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i LOCATION: 324
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4306
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US-09-814-353-4306/c
; Sequence 4306, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Lillie, James
; TITLE OF INVENTION: Pamela
; TITLE OF INVENTION: DEDITION, AND METHODS FOR
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US 60/191,031
; PRIOR PILING DATE: 2000-03-21
; PRIOR PLING DATE: 2000-03-25
; PRIOR PLING DATE: 2000-05-25
; PRIOR PLING DATE: 2000-06-15
; PRIOR PLING DATE: 2000-06-15
; PRIOR PLING DATE: 2000-07-07
; PRIOR PL
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GENERAL INFORMATION:

APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITILE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
FRIOR APPLICATION NUMBER: US 60/191,031
FRIOR FILING DATE: 2000-03-21
FRIOR PRILING DATE: 2000-03-21
FRIOR APPLICATION NUMBER: US 60/211,940
FRIOR APPLICATION NUMBER: US 60/216,820
FRIOR APPLICATION NUMBER: US 60/216,820
FRIOR APPLICATION NUMBER: US 60/226,61
FRIOR FILING DATE: 2000-07-07
FRIOR APPLICATION NUMBER: US 60/257,672
FRIOR FILING DATE: 2000-07-25
FRIOR APPLICATION NUMBER: US 60/257,672
FRIOR FILING DATE: 2000-012-21
FRIOR FILING DATE: 2000-012-3
FRIOR FILING DATE: 2000-012-3
FRIOR FILING DATE: 2000-012-3
FRIOR FILING DATE: SUBJECT WINDOWS VERSION 4.0
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 36059, Application US/10357930

Sequence 36059, Application No. US20040259086A1

SEQUENCE SEQUENCE SEQUENCE

APPLICANT: Schlegel. Robert

APPLICANT: Badege, WA18on

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: UNINAL OF UNINAL OF USE CANCER

TITLE OF UNENTION: UNINAL OF USE CANCER

CURRENT APPLICATION NUMBER: US/10/357,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10610, Application US/09814353

Sequence 10610, Application US/09814353

Publication No. U520030165831A1

GENERAL INPORMATION:

APPLICANT: Leb. John

APPLICANT: Lillie, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: NOWBER: US/09/814,353

CURRENT APPLICATION NUMBER: US/09/814,353

CURRENT FILING DATE: 2001-03-21

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-25
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                                                                                        0; Indels
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DB 3;
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1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
Query Match

1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                   30 TAAGTACCTCGGCCGCGACCACGC 7
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71 TAAGTACCTCGGCGCGCACCACGC 48
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Sequence 37991, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Schlegel. Robert
APPLICANT: Bradege, Wilson
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: 10978C3
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-04
PRIOR FILING DATE: 2000-03-16
PRIOR PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-07-18
PRIOR PRILING DATE: 2000-07-18
PRICE PRILING DATE: 2000-07-18
PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.4%; Score 24; DB 8; Length 446; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 24; Conservative 0; Mismatches 0; Indels
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1.4%; Score 24; DB 8;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR PILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/189,319
PRIOR PILING DATE: 2000-02-17
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PASSES FOR WINDOWS VERSION 4.0
SSOFTWARE: PASSES FOR WINDOWS VERSION 4.0
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CORGANISM: Homo sapiens
US-10-357-930-37991
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US-10-357-930-37991/c
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APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Sun, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
FILE REFERENCE: DEX-0273
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin version 3.1
SEQ ID NO 66
                                                                                                                                                                                                          APPLICANT: SCHLEGE, Wilson
APPLICANT: Budege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES,
TITLE OF INVENTION: DIDENTIFICATION, AND THERAPY OF
TITLE OF INVENTION: UNDERS: CANCER
TITLE OF INVENTION: UNDERS: 09/10/57,930
CURRENT APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-18
PRIOR FILING DATE: 2000-07-18
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1.4%; Score 24; DB 8;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
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                                                                  Sequence 45120, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 TAAGTACCTCGGCCGCGACCACGC 78
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US-10-001-857-66/c
; Sequence 66, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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US-10-001-857-66
RESULT 75
US-10-357-930-45120/c
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Length 463; Indels

DB 5; 0.13;

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; TYPE: DNA

; GCGANISH: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 18, 43, 86, 89, 264, 388, 407, 432

;; OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                 Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 24; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 79
US-09-814-353-3344/C
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US-10-198-846-5501/C
US-10-198-846-5501, Application US/10198846

Publication No. US20030099974A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR SEQ ID NOS: 14008
SOFTWARE: FREESE FEELESE FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                    WES-09-614-353-18705/C

Sequence 18705, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: OF 001-001-01

FILE REPERENCE: MRI-006B

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/207,124

PRIOR FILING DATE: 2000-05-25

PRIOR PELING DATE: 2000-06-15

PRIOR PELING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: US 60/216,820

PRIOR PELING DATE: 2000-07-07

PRIOR PELING DATE: 2000-07-07

PRIOR PELING DATE: 2000-07-07

PRIOR PELING DATE: 2000-07-22

PRIOR PELING DATE: 2000-07-22

PRIOR PELING DATE: 2000-07-25

PRIOR PELING DATE: 2007-07-25

PRIOR PELING DATE: 2007-07-25

PRIOR PELING DATE: 2007-07-2
                                                                             Gaps
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Score 24; DB 5; Length 457;
Pred. No. 0.13;
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                                                                             0; Indels
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Query Match 1.4%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 24; Conservative 0; Mismatches
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1.4%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 24; Conservative 0; Mismatches
                                                                                                                                                  1690 TAAGTACCTCGGCCGCGACCACGC 1713
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Gaps
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LOCATION: 99, 279, 300, 303, 315, 331, 344, 352, 356, 371, 377, 380,
LOCATION: 383, 393, 417, 422, 428, 431
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lee, John
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
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1.4%; Score 24; DB 3; Length 464;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION UNWBER: US 60/191,031
PRIOR PILLING DATE: 2000-03-21
PRIOR PILLING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-1-21
NUMBER OF SEQ ID NOS: 22037
SEQ ID NO 3344
PURPLE PASSED FOR WINDOWS VERSION 4.0
                                                         1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                     116 TAAGTACCTCGGCCGCGACCACGC 93
                                                                                                                                                                                                                                                                         Sequence 3344, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
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; Publication No. US20030165831A1
; GENERAL INFORMATION:
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APPLICANT: Thompson, Pame
APPLICANT: Lillie, James
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RESULT 83
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US-09-814-353-15851/c

Sequence 15851, Application US/09814353

Publication No. US20030165831A1

GENERAL INPORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: TILLIE, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MRI-006B

CURRENT FILING DATE: 2010-03-21

PRIOR PRIOR PLICATION NUMBER: US 60/191,031

PRIOR PLICATION NUMBER: US 60/201,124

PRIOR PLILING DATE: 2000-05-25

PRIOR PLILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR PLILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-07-07

PRIOR PLILING DATE: 2000-07-07

PRIOR FILING DA
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND FILL OF INVENTION: THERAPY OF OVARIAN CANCER FILL REFERENCE: MRI-006B

CURRENT FILLNG DATE: 2001-03-21

PRIOR PLICATION NUMBER: US 60/191,031

PRIOR PLICATION NUMBER: US 60/207,124

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-06-15

PRIOR PLICATION NUMBER: US 60/211,940

PRIOR PLICATION NUMBER: US 60/216,820

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-07-25

PRIOR PLING DATE: 2000-07-25
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; LOCATION: 99, 279, 300, 303, 315, 331, 344, 352, 356, 371, 377, 380,

; LOCATION: 383, 393, 403, 417, 422, 428, 431

; COTHER INFORMATION: n = A,T,C or G

US-09-814-353-9665
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1.4%; Score 24; DB 3; Length 464;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: 2001-03-21
CURRENT APPLICATION NUMBER: US 60/201, 124
PRIOR PELICATION NUMBER: US 60/201, 124
PRIOR PELICATION NUMBER: US 60/211, 940
PRIOR PELICATION NUMBER: US 60/211, 940
PRIOR PELICATION NUMBER: US 60/216, 820
PRIOR PELICATION NUMBER: US 60/216, 820
PRIOR PELICATION NUMBER: US 60/220, 661
PRIOR
                                                                                                    Gaps
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Sequence 10775, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: WII-0068
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
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NAME/KEY: misc_feature

LOCATION: 31, 98, 159, 166, 289, 348, 361, 364, 385, 393, 398, 400,

LOCATION: 403, 410, 414, 419, 432, 457, 467

OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4472
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1.4%; Score 24; DB 3; Length 486;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
Query Match
1.4%; Score 24; DB 3; Length 471;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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US-09-814-353-4472/c
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Sequence 4993, Application US/09814353
| Sequence 4993, Application US/09814353
| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lee, John
| APPLICANT: Thompson, Pamela
| APPLICANT: Thompson, Pamela
| APPLICANT: Library OF OVARIAN CANCER ITTLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND ITTLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND ITTLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND ITTLE OF INVENTION: MAILOGE OF USE OF OUR STATE STIL OF DATE: 2001-03-21
| PRIOR PLLING DATE: 2001-03-21
| PRIOR PLLING DATE: 2000-03-21
| PRIOR PLLING DATE: 2000-05-25
| PRIOR PLLING DATE: 2000-06-15
| PRIOR PLLING DATE: 2000-07-07, PRIOR PLUB PRIOR PRIOR PLUB PRIOR PLUB PRIOR PLUB PRIOR PLUB PRIOR PLUB PRIOR PRIOR PLUB PRIOR PLUB PRIOR P
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100.0%; Pred. No. 0.13;
tive 0; Mismatches 0; Indels
                     0; Indels
                 0; Mismatches
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Best Local Similarity 100.0
Matches 24; Conservative
                 24; Conservative
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US-09-814-353-15976/c
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US-09-814-353-4993/C
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APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERENCE: MXI-006B
CURRENT PILLING DATE: 2001-03-21
PRIOR FILLING DATE: 2000-03-21
PRIOR PILLING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-25
PRIOR PLILING DATE: 2000-05-25
PRIOR PLILING DATE: 2000-05-15
PRIOR PILLING DATE: 2000-06-15
PRIOR PILLING DATE: 2000-06-15
PRIOR PILLING DATE: 2000-07-07
PRIOR PILLING DATE: 2000-07-22
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; NAME/KEY: misc feature

; LOCATION: 31, 98, 159, 166, 289, 348, 361, 364, 385, 393, 398, 400,

; LOCATION: 403, 410, 414, 419, 432, 457, 467

; OTHER INFORMATION: n = A,T,C or G

US-09-814-353-10775
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 10775
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Publication No. US20030165831A1
GENERAL INFORMATION:
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US-09-814-353-16367
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US-09-814-353-16367/c
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Sequence 11286, Application US/09814353

Publication No. US2030165831A1

GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, APPLICANT:
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, APPLICANT:
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: OF THE STEEL OF ONCE OF THE STEEL OF TH
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1.4%; Score 24; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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1.4%; Score 24; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 4993
LENGTH: 521
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LOCATION: 443, 491
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 443, 491

COTHEN INFORMATION: n = A,T,C or G

US-09-814-353-11286
                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-814-353-11286/c
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RESULT 88 US-09-814-353-15615/c

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| Publication No. U82001165911A1
| Sequence 1567, Application U8 (09814353)
| GREERAL INPORTATION:
| The Comment of the Commen
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US-09-814-353-17394
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
                                                                                                                                                                                                                                                  Query Match 1.4%; Score 24; DB 3; Length 524; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 24; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           1690 TAAGTACCTCGGCCGCGACCACGC 1713
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
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                                                                                  ; LOCATION: 350
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-17892
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; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5823
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Best Local Similarity 100.0
Matches 24; Conservative
FEATURE:
NAME/KEY: migc_feature
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US-09-814-353-12105/c
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US-09-814-353-5823/c
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A STANDARD

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US-10-357-3910-3916/C
US-10-357-3910-3916/C
Publication No. US20040259086A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION WINGER:
CURRENT APPLICATION WINGER: US/10/357,930
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR PRIOR PRIOR PRIOR DATE: 2000-01-18
PRIOR PRIOR PRING DATE: 2000-01-18
PRIOR PRIOR PRING DATE: 2000-01-18
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1.4%; Score 24; DB 8; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.13;
tive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SCOTTWARE: 548
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NAME/KEY: misc_feature

LOCATION: 388, "442, 468, 478, 503, 540

CTHER INFORMATION: n = A,T,C or G
US-09-814-353-12321
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Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-09-814-353-6042/C

| Sequence 6042, Application US/09814353
| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lee, John
| APPLICANT: Lee, John
| APPLICANT: Lille, James
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| FRICK FILING DATE: 2000-03-21
| PRIOR APPLICATION NUMBER: US 60/201, 940
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-07-07
| PRIOR FILING DATE: 2000-07-07
| PRIOR PRILING DATE: 2000-07-07
| PRIOR APPLICATION NUMBER: US 60/216,820
| PRIOR FILING DATE: 2000-07-07
| PRIOR FILING DATE: 2000
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MAI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US/09/814,353
FILE REPERENCE: MAI-006B
PRIOR APPLICATION NUMBER: US/09/814,353
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
                                                                                                                                            Gaps
                                             Query Match 1.4%; Score 24; DB 3; Length 546; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 24; Conservative 0; Mismatches 0; Indels
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Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                   1690 TAAGTACCTCGGCCGCGACCACGC 1713
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                                                                                                                                                                                                                                                                                                                    105 TAAGTACCTCGGCCGCGACCACGC 82
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US-09-814-353-12321/c
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RESULT 99
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                                                                                                                                                                                   Sequence 43996, Application US/10357930

Sequence 43996, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel. Robert

APPLICANT: Bendese, Wilson

APPLICANT: Bendese, Wilson

APPLICANT: Bendese, Wilson

APPLICANT: Monahan, John

ITILE OF INVENTION: NUBER: US/10, ASESSMENT, PREVENTION, AND THERAPY OF

ITILE OF INVENTION: UDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

ITILE OF INVENTION: UNMER: US/10, 330

CURRENT APPLICATION NUMBER: 09/785, 276

PRIOR APPLICATION NUMBER: 09/185, 276

PRIOR PILING DATE: 2000-02-17

PRIOR PILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/183, 319

PRIOR APPLICATION NUMBER: 60/183, 319

PRIOR PILING DATE: 2000-03-16

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-07-18

PRIOR DATE: 2000-07-18

PRIOR PILING DATE: 2000-07-18

PRIOR PILING DATE: 2000-07-18

PRIOR PILING DATE: 2000-07-18

PRIOR
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| Publication No. US20030165831A1 |
| GENERAL INFORMATION: |
| APPLICANT: Lee, John |
| APPLICANT: Thompson, Pamela |
| APPLICANT: Lillie, James |
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR |
| TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER |
| FILE REFERENCE: MRI-0.068 |
| CURRENT APPLICATION NUMBER: US 60/191,031 |
| PRIOR PRILING DATE: 2000-03-21 |
| PRIOR PILLING DATE: 2000-05-25 |
| PRIOR APPLICATION NUMBER: US 60/211,940 |
| PRIOR APPLICATION NUMBER: US 60/211,940 |
| PRIOR APPLICATION NUMBER: US 60/211,940 |
| PRIOR APPLICATION NUMBER: US 60/210,661 |
| PRIOR APPLICATION NUMBER: US 60/220,661 |
| PRIOR APPLICATION NUMBER: US 60/220,661 |
| PRIOR APPLICATION NUMBER: US 60/220,661 |
| PRIOR APPLICATION NUMBER: US 60/257,672 |
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85 TAAGTACCTCGGCCGCGACCACGC 62
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US-09-814-353-18489/c
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Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSITIONS, KITS, AND METHODS FOR ASSESSMENT, PREVENTION, AND THERAPY OF
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                                                                                                                                                                                                                                                                       Length 601;
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1.4%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36049, Application US/10357930
Publication No. US20040259086A1
GENERAL INPORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: IDENTIFICATION, ASSESSME)
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILLE REFERENCE: MR.-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT PILING DATE: 2003-02-04
PRIOR PILING DATE: 2000-02-16
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR PILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PRILING DATE: 2000-07-18
PRIOR PRILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
NUMBER OF SEQ ID NOS: 62232
LENGTH: 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOSITIONS,
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 18489
LENGTH: 601
TYPE: DNA
ORGANISM: Homo sapiens
US-09-814-353-18489
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ORGANISM: Homo sapiens
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US-10-357-930-36049
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US-10-956-009-112/c
; Sequence 112, Application US/10950009
; Publication No. US2005066994A1
; GENERAL INFORMATION:
APPLICANT: BERKA, Randy
; APPLICANT: BASHKINOVA, Elena
APPLICANT: REY, Michael
; TITLE DOF INVENTION: Methods For Monitoring Gene Expression
FILE REPERBNCE: 10541.200-US
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 05/50,140
PRIOR APPLICATION NUMBER: 60/506,140
PRIOR PILING DATE: 2003-09-25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 112
LENGTH: 610
; TYPE: DNA
TYPE: 
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1.4%; Score 24; DB 8; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
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1.4%; Score 24; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: HUMAN PROSTATE CANCER FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/786,276
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FLING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/189, 862
PRIOR APPLICATION NUMBER: 60/21,454
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SEQ ID NO 45110
LENGTH...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-357-930-45110
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Search completed: March 11, 2006, 22:31:51 Job time : 1455 secs

Perfect score:

Sequence:

Word size

Database

Searched:

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Sequence 1045313, Sequence 1045313, Sequence 1045313, Sequence 1045329, Sequence 1045329, Sequence 1045330, Sequence 1045331, Sequence 1045331, Sequence 1045331, Sequence 1045312, Sequence 193849, Sequence 193849, Sequence 193849, Sequence 193849, Sequence 193849, Sequence 194531, Sequence 194531, Sequence 194531, Sequence 194531, Sequence 194531, Sequence 1045331, Sequence 1045321, Sequence 1045331, Sequence 1045335, Sequence 1430755, Sequence 1430759, Sequence 1430759, Sequence 1430759, Sequence 1430759, Sequence 1430759, Sequence 1430761, Sequ
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Sequence 1430763,
Sequence 1430764,
Sequence 1430765,
Sequence 1430765,
Sequence 1430767,
Sequence 344523,
Sequence 344524,
Sequence 344526,
Sequence 344526,
Sequence 1045318,
Sequence 1045318,
Sequence 1045311,
Sequence 1045311,
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Sequence 1430773,
Sequence 1430774,
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Sequence 1430770
Sequence 1430771
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Sequence 1
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Sequence
Sequence
                                                                                                                     US-10-310-914A-1045327

US-10-310-914A-1045327

US-10-310-914A-10453105

US-10-310-914A-10453105

US-10-310-914A-1045310

US-10-310-914A-1045310

US-10-310-914A-10453110

US-10-310-914A-1045313

US-10-310-914A-1045331

US-10-310-914A-1045313

US-
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      Sequence 799, App
Sequence 1045304,
Sequence 1045320,
Sequence 344330,
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Sequence 344333,
Sequence 344334,
Sequence 344336,
Sequence 344336,
Sequence 344337,
Sequence 3444138,
Sequence 344517,
Sequence 344512,
Sequence 344512,
Sequence 344512,
Sequence 344512,
Sequence 344512,
                                                                                                       March 11, 2006, 21:01:03; Search time 679 Seconds (without alignments) 5820.912 Million cell updates/sec
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1713
1 atgccccgccctggacaccc......tacctcggccgcgaccacgc 1713
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1. /cgn2 6/ptodata/2/pubpna/USOB NEW PUB.seq:*
2. /cgn2_6/ptodata/2/pubpna/USOB NEW_PUB.seq:*
3. /cgn2_6/ptodata/2/pubpna/USOB NEW_PUB.seq:*
4. /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
5. /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
6. /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
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7. /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
9. /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
9. /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
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12. /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
13. /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-310-914A-1045304
US-10-310-914A-10453204
US-11-121-849-344331
US-11-121-849-344331
US-11-121-849-344332
US-11-121-849-344333
US-11-121-849-344334
US-11-121-849-344335
US-11-121-849-344336
US-11-121-849-344339
US-11-121-849-344339
US-11-121-849-344518
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                                                                                                                                                                                                                                                                          7673375 seqs, 1153648444 residues
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                                                                            nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length
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Score

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Sequence 1430777, Sequence 1430778, Sequence 1430780, Sequence 1430781,	equence 14	equence 14	equence 14	equence 14	equence 14	equence 14	equence 14	equence 14	equence 14	equence 14	equence 14	equence 14	14	equence 14	equence 14	equence 14	equence 14	equence 14	oducino 14	equence 14	eduence 14	equence 14	equence 14	equence 14	equence 14	equence 14	equence 14	AL ADIRACES	7 7	emience 14	equence 14	equence 14	emience 14	equence 14	equence 14	equence 14	equence 14	equence 11	equence 44	equence 19	equence 41	equence 6,	equence 57	equence 66	equence 29	equence 6,	Seguence 60	equence 140	ence 139	equence 141	equence 145	Sequence 56	sence 62	ALA annaima	equence ortizes,	equence 4047,	equence 52110	equence 88170	Sequence 515849,	equence 51585	equence 84479	equence 88460	equence 88460 empande 91057					
US-11-083-784-1430777 US-11-083-784-1430778 US-11-083-784-1430780 US-11-083-784-1430781	083-784-143	.083-784-143	083-784-143	.083-784-143	.083-784-143	.083-784-143	083-784-143	083-784-143	083-784-143	.083-784-143	083-784-143	.083-784-143	.083-784-143	083-784-143	083-784-143	.083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	EAL-207-500.	083-784-143	.083-784-143	.083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	2007-104-143	. 003-704-143	083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	083-784-143	031-356-11	.063-	136-	.063-	.031-	108-	108-	.234-	108-	US-11-108-	S-10-623-1	23-1	S-10-623-1	S-10-623-1	US-11-108-	108-	2-02-02-0	0 20 00 0	0-076-60-6	8-09-325-0	8-09-925-0	US-09-925-065A-515849	S-09-925-0	S-09-925-0	8-09-925-0	0-626-60-6
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; Publication No. US2006000332A1
; GENERAL INPORMATION:
APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectal
; TITLE OF INVENTION: Bioinformatically detectal
; FILE REPERENCE: 060037.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
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CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 799
                                                                                                                                                                   Query Match 93.1%;
Best Local Similarity 99.9%;
Matches 1694; Conservative 0
                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                                                                       LENGTH: 1785
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1469 1440 1529 1500 1589 1560

1620 1649

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Sequence 344331, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

TITLE OF INVENTION:

MICROGRAPH US/11/121,849

FILE REFERENCE: 3684.1

CURRENT FILING DATE: 2005-05-03

RIGHT PELING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SEQ ID NO 344331

LENGTH: 25
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Publication No. US20050272080A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.11
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 06/567,949
PRIOR APPLICATION NUMBER: 06/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ ID NO 344332
LENGTH: 25
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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
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100.0%; Pred. No. 0.028;
tive 0; Mismatches 0
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; Sequence 344333, Application US/11121849
; Publication No. US20050272080A1
    1 CTGGACCATGTGCATTTCACTGGGC 25
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Best Local Similarity 100.
Matches 25; Conservative
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Matches 25; Conservative
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COGANISM: Homo sapien
US-11-121-849-344332
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CORGANISM: Homo sapien
US-11-121-849-344331
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Publication No. US20060003322A1
Publication No. US20060003322A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUBBR: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045320
LENGTH: 25
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Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Macroarrays
FILE OF INVENTION: Macroarrays
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
SEQ ID NOS: 673904
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100.0%; Pred. No. 0.028;
tive 0; Mismatches 0
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NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatenIn version 3.3
SEQ ID NO 1045304
LENGTH: 25
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Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity 100.
Matches 25; Conservative
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US-11-121-849-344330
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US-10-310-914A-1045320/c
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                                                                                           TYPE: RNA
ORGANISM: Human
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Sequence 344336, Application US/11121849
Sequence 344336, Application US/11121849
Publication No. US20050272080A1
Sequence 344336, Application Sequence 344336, Application US/11121849
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Septime Introde TNVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TILLE OF INVENTION: Microarrays
TILLE OF INVENTION: Microarray Septime Sequence Listing Generator V 1.1
SEQ ID NOS: 673904
SEQ ID NOS: 673904
SEQ ID NO 344336
LENGTH: 25
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Publication No. US20050272080A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded SE
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR PEDILORIUS DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 344337

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       Indels
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       0; Mismatches
                                                  1466 AGGAGTTAGGCATTACCTTCTGGGA 1490
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; Sequence 344338
; Publication No. US20050272080A1
; GENERAL INPORMATION:
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    25; Conservative
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US-11-121-849-344336
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CORGANISM: Homo sapien
US-11-121-849-344337
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US-11-121-849-344337
    Matches
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Sequence 344334, Application US/11121849
Publication No. US20050272080A1
Sequence 344334
Sequence 144334
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Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Microarrays
TITLE OF INVENTION:
Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT PILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344335
LENGTH: 25
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CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344333
LENGTH: 25
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100.0%; Pred. No. 0.028;
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Best Local Similarity 100.(
Matches 25; Conservative
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Matches 25; Conservative
                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapien
US-11-121-849-344333
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CORGANISM: Homo sapien
US-11-121-849-344334
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CORGANISM: Homo sapien
US-11-121-849-344335
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Best Local Similarity
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US-11-121-849-344335
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US-11-121-849-344334
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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR PILING DATE: 2005-05-03
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344517
LENGTH: 25
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Publication No. US20050272080A1
GENERAL INFORMATION
APPLICANT: John Palma
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR PILING DATE: 2005-05-03
PRIOR FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
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                                                        1.5%; Score 25; DB 12; Length 25; 100.0%; Pred. No. 0.028; ive 0; Mismatches 0; Indels
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344518
LENGTH: 25
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0.028;
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100.0%; Pred. No. 0.028;
tive 0; Mismatches 0
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                                                                                                                                                     1318 TCCTGCCTTGGCTGACTGGGTTCCT 1342
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                                                                                                                                                                             1 TCCTGCCTTGGCTGACTGGGTTCCT 25
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Publication No. US20050272080A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 25; Conservative
                                                        Query Match 1.5
Best Local Similarity 100.
Matches 25; Conservative
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CORGANISM: Homo sapien
US-11-121-849-344517
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US-11-121-849-344518
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US-11-121-849-344519
            US-11-121-849-344340
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Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Microarrays
FILE REPERENCE: 368410ATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344339
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded FILE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 344338

LENGTH: 25
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US-11-121-849-344340
US-11-121-849-344340, Application US/11121849
Publication No. US205050272080A1
Publication No. US205050272080A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
NUMBER OF SEQ ID NOS: 673904
SOSTWARE: Microarray Probe Sequence Listing Generator V 1.1
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100.0%; Pred. No. 0.0
ive 0; Mismatches
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Matches 25; Conservative
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Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344338
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; ORGANISM: Homo sapien
US-11-121-849-344339
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-11-121-849-344339
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LENGTH: 25
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Publication No. US20050272080A1

SENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT PILING DATE: 2005-05-03
PRIOR PILICATION NUMBER: 60/567,949
PRIOR PILICATION NUMBER: 60/567,949
PRIOR PILICATION NUMBER: 60/567,949
SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
LENGTH: 25
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Fublication No. US20050272080A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
FILE REFRENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

FILOR PELICATION NUMBER: 06/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SEQ ID NO 344523

LENGTH: 25
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                                                                                                                                                1.5%; Score 25; DB 12; Length 25; 100.0%; Pred. No. 0.028; tive 0; Mismatches 0; Indels
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Matches 25; Conservative
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Best Local Similarity 100.
Matches 25; Conservative
                                                     TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-344521
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US-11-121-849-344522
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US-11-121-849-344523
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US-11-121-849-344522
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         ; SEQ ID NO 344521
; LENGTH: 25
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Sequence 344519, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Mcroarrays
TITLE OF INVENTION: Mcroarrays
FILE REPERBNCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 345519
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US-11-121-849-344520
US-11-121-849-344520
Sequence 344520, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded (FILE REFERENCE: 3684.1)
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION UMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
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llarity 100.0%; Pred. No. 0.028;
Conservative 0; Mismatches 0; Indels
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 34520
LENGTH: 25
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US-11-121-849-344521
; Sequence 344521, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 25; Conservative
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; ORGANISM: Homo sapien
US-11-121-849-344519
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US-11-121-849-344520
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Best Local Similarity
Matches 25; Conserv
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Sequence 344527, Application US/11121849
Sequence 344527, Application US/11121849
Sequence 344527, Application No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Statics OF INVENTION: Microarrays
TITLE OF INVENTION:
MICROBALICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
FILOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ ID NO 344527
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 25;
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 344526
LENGTH: 25
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Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344526
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CORGANISM: Homo sapien
US-11-121-849-344527
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US-10-310-914A-1045318/C
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; ORGANISM: Human
US-10-310-914A-1045318
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                                                                                                                                    Sequence 344524, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
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Publication No. U320050272080A1
GENERAL INFORMATION:
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100.0%; Pred. No. 0.028;
:ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 25; Conservative
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Matches 25; Conservative
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US-11-121-849-344524
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; ORGANISM: Homo sapien
US-11-121-849-344525
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US-11-121-849-344525
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Sequence 104537, Application US/10310914A
Publication No. US20060003322A1
FEBREAL TRFORMATION:
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 1045327
LENGTH: 23
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Publication No. US20060003322A1
Publication No. US2006000332A1
Publication No. US200600032A1

REDERAL INPORMATION:
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FAPILICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 1045337
LENGTH: 23
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CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3 SEQ ID NO 1045322 LENGTH: 23
                                                                                                                                                                                                                                                                                                               1593 TTGTATTGGGGGGTGGGCAGGGC 1615
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                                                                                                                                               Sequence 1045328, Application US/10310914A
Sequence 1045328, Application US/10310914A
Publication No. US20060003322A1
GENERAL INPORMATION:
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION UNMERE: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NOS: 1388402
SEQ ID NOS: 1388402
SEQ ID NOS: 2002-12-06
LENGTH: 24
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL THORMATION:
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: USES thereof
FILER REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
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100.0%; Pred. No. 0.093;
ive 0; Mismatches 0; Indels
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Pred. No. 0.3;
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  1378 ATCTCCTTGCATCCCCAGCTGGTC 1401
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Best Local Similarity 100.
Matches 24; Conservative
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Best Local Similarity 100.
Matches 23; Conservative
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US-10-310-914A-1045328/c
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US-10-310-914A-1045322/c
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US-10-310-914A-1045311/c
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; ORGANISM: Human
US-10-310-914A-1045328
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; ORGANISM: Human
US-10-310-914A-1045311
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US-10-310-914A-1045309/c

US-10-310-914A-1045309/c

Sequence 1045309, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Biller, KVUZat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: USEs thereof

FILE REFERENCE: 66087.0200.CPUS01

CURRENT APPLICATION VUMBER: US/10/310,914A

CURRENT APPLICATION VUMBER: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1045309

LENGTH: 22
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, 1saac
APPLICANT: Bentwich, 1saac
APPLICANT: Bentwich, 1saac
APPLICANTON: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045310
LENGTH: 22
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100.0%; Pred. No. 0.99;
tive 0; Mismatches 0; Indels
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0.99;
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Pred. No.
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CURRENT FILING DATE: 2002-12-C
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045307
LENGTH: 22
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 22; Conservative
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US-10-310-914A-1045310/c
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US-10-310-914A-1045309
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                                                                                                                                                                                                                    Query Match
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US-10-914A-1045307/C
US-10-310-914A-1045307/C

is Sequence 10453307, Application US/10310914A

is Sequence 10453307, Application US/2066003322A1

is GENERAL INFORMATION:
is APPLICANT: Shiler, Kuzat
is TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and ITILE OF INVENTION: uses thereof
if TITLE OF UNDERTION NUMBER: US/10/310,914A
                                                                                          RESULT 32
US-10-314A-1045303/c
US-10-310-914A-1045303/c
Sequence 1045303, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
CURRENT PRILIATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045303
LENGTH: 22
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APPLICANT: Baller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045306
LENGTH: 22
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0.99;
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100.0%; Pred. No. v...
... 0; Mismatches
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  TGTGGGAGAGGCTTAGACCTGAA
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Best Local Similarity 100.
Matches 22; Conservative
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US-10-310-914A-1045306/c
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Best Local Similarity
Matches 22; Conserv
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US-10-310-914A-1045306
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Sequence 1045319, Application US/10310914A

Publication No. US2006000332A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Biller, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1045319

LENGTH: 22
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Publication No. US2060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045323
LENGTH: 22
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100.0%; Pred. No. 0.99;
iive 0; Mismatches
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100.0%; Pred. No. ...
0; Mismatches
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1.3%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 0.5
Matches 22; Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045315
LENGTH: 22
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Best Local Similarity 100.0
Matches 22; Conservative
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Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                  CRGANISM: Human
US-10-310-914A-1045315
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ORGANISM: Human
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ORGANISM: Human
                                                                                                  TYPE: RNA
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 066087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOPTWARE: PatentIn version 3.3
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUSOI
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: Patentin version 3.3
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06697-0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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100.0%; Pred. No. 0.99;
tive 0; Mismatches 0; Indels
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                                                                 RESULT 37
US-10-310-914A-1045313/c
US-10-310-914A-1045313, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Tieaac
; APPLICANT: Shiler, Kvuzat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1045314, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION: APPLICANT: Bentwich, Isaac
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  CTGTGGGAGAGGCTTAGACCTG
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Best Local Similarity 100.4
Matches 22; Conservative
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Matches 22; Conservative
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US-10-310-914A-1045314/c
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US-10-310-914A-1045315/c
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LENGTH: 22
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LENGTH: 22
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US-10-310-914A-1045332/c

US-10-310-914A-1045332, Application US/10310914A

Sequence 104532, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

CURRENT APPLICATION VNMBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 1045332

LENGTH: 22
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045305
LENGTH: 21
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100.0%; Pred. No. 3.2;
                                                                                                                                            Length 22;
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                                                                                                                                                                                            0; Indels
                                                                                                                                            Query Match 1.3%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 0.5 Matches 22; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 22; Conservative
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Matches 21; Conservative
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US-10-310-914A-1045305/c
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ORGANISM: Human
SEQ ID NO 1045330
LENGTH: 22
                                               TYPE: RNA
ORGANISM: Human
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Publication No. US20060003322A1
Publication No. US2006000322A1
Publication No. US2006000322A1
Publication No. US2006000322A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Wuzat
APPLICANT: Shiler, Wuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION UNDER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1045329
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1045330, Application US/10310914A
Publication No. US20060003322A1
Publication No. US20060003322A1
Publication No. US2006000322A1
Publication No. US2006000322A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICANTON NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                 APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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100.0%; Pred. No. 0.99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Prec.
                                                                   Sequence 1045324, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT:
BELLYMICH, ISSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1439 CTTCAGGTGGCCTGATCATGGA 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 GGGCCATGGGATCTACATCTCC 1
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Matches 22; Conservative
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US-10-310-914A-1045329/c
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US-10-310-914A-1045330/c
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LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
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APPLICANT: Xu, Dongwei

APPLICANT: Xu, Dongwei

APPLICANT: Nielsen, Mark T.

TITLE OF INVENTION Niccitean Nucleic Acid Molecules and Uses Thereof

FILE REFERENCE: 07678/141014

CURRENT APPLICATION NUMBER: 05/65,451

PRIOR APPLICATION NUMBER: 60/665,097

PRIOR APPLICATION NUMBER: 60/665,097

PRIOR APPLICATION NUMBER: 60/665,097

PRIOR FILING DATE: 2005-03-24

PRIOR FILING DATE: 2006-03-24

PRIOR FILING DATE: 2004-09-03

PRIOR PLILING DATE: 2004-09-17

PRIOR PPLICATION NUMBER: 60/503,989

PRIOR PLILING DATE: 2003-09-18

PRIOR PLILING DATE: 2003-10-16

PRIOR PLILING DATE: 2005-10-16

PRIOR PLILING DATE: 2005-10-16
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PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR FILING DATE: 1998-02-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 701
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 301
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100.0%; Pred. No. 3.6;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2005, Application US/11116881A Publication No. US20060041949A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 992, Application US/11116881A
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                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100. Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                        / TYPE: DNA
/ ORGANISM: Homo sapien
US-11-234-786-293
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US-11-116-881A-2005
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US-11-116-881A-992
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APPLICANT: Skeiky, Yasir A.
TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: POLYPEPTIDES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 8; Length 21;
Pred. No. 3.2;
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100.0%; Pred. No. ...
0; Mismatches
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CURRENT APPLICATION NUMBER: US/11/234,786
CURRENT FILING DATE: 2005-09-23
PRIOR PLICATION NUMBER: US 09/568,857
PRIOR PLICATION NUMBER: US 09/568,857
PRIOR PILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 09/483,672
PRIOR APPLICATION NUMBER: US 09/483,672
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/352,616
PRIOR PILING DATE: 1999-07-13
PRIOR PILING DATE: 1999-01-15
PRIOR PILING DATE: 1999-01-15
PRIOR PULING DATE: 1999-01-15
PRIOR PILING DATE: 1999-01-15
PRIOR PILING DATE: 1999-01-15
PRIOR PILING DATE: 1998-02-23
PRIOR PILING DATE: 1998-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 233, Application US/11234786; Publication No. US20060024301A1
SPUBRAL INFORMATION:
APPLICANT: Vi, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Aiang, Yuqiu
APPLICANT: Reed, Steven G.
APPLICANT: Reade, Steven G.
APPLICANT: Ranger, Gary R.
APPLICANT: Ranger, Gary R.
APPLICANT: Rather, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Usedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1509 CCCCTATTGCCACCCTAACCA 1529
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Best Local Similarity 100.
Matches 21; Conservative
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ORGANISM: Human
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مهومية ممائلة

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FEATURE:
NAME/KEY: misc_feature
LOCATION: (37)...(37)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (40)...(41)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (40)...(43)
OTHER INFORMATION: n is a, c, g, or t
OTHER INFORMATION: n is a, c, g, or t
OTHER INFORMATION: n is a, c, g, or t
                             1693 GTACCTCGGCGCGCACCA 1713
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                                                                                    24 GIACCICGGCCGCGACCACGC 4
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Matches 21; Conserva
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                                     APPLICANT: Xu. Dongmei;
APPLICANT: Xu. Dongmei;
APPLICANT: Nielsen, Mark T.
TITLE OF INVENTION: Niccitiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT PILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: 60/665,451
PRIOR APPLICATION NUMBER: 60/665,097
PRIOR APPLICATION NUMBER: 60/665,097
PRIOR APPLICATION NUMBER: 60/665,097
PRIOR PILING DATE: 2005-01-25
PRIOR PILING DATE: 2005-01-25
PRIOR FILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 2300 SOFTWARE: PatentIn version 3.3 SEQ ID NO 992
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US-11-057-484A-13/C

Sequence 13, Application US/11057484A

Publication No. US2006002931A1

GENERAL INFORMATION:

APPLICANT: Finkel, Terri H.

APPLICANT: Finkel, Terri H.

TITLE OF INVENTION:

TITLE OF INVENTION: Telection and Methods of Use Thereof

FILE REFERENCE: CHOP: 0.146CIP

CURRENT APPLICATION NUMBER: US/11/057,484A

CURRENT PILING DATE: 2005-02-14

PRIOR FILING DATE: 2003-02-19

PRIOR FILING DATE: 2003-02-19

PRIOR FILING DATE: 2003-02-19

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FRASESEQ for Windows Version 3.0

SEQ ID NO 13

LENGTH: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2%; Score 21; DB 9; Length 405;
100.0%; Pred. No. 3.6;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.6;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1693 GTACCTCGGCCGCGACCACGC 1713
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Publication No. US20060041949A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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; ORGANISM: Homo sapien
US-11-057-484A-13
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Matches 21; Conserv
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RESULT 53
US-11-206-587-4/C

Sequence 4, Application US/11206587
Publication No. US20060040306A1
GENERAL INFORMATION:
THE OF INVENTION: 14544 METHODS AND COMPOSITIONS OF HUMAN PROTEINS APPLICANT: THERE OF INVENTION: 14544 METHODS AND COMPOSITIONS OF HUMAN PROTEINS OF TITLE OF INVENTION: 14544 METHODS AND COMPOSITIONS OF HUMAN PROTEINS OF HUMAN PRICE STILLS OF INVENTION: 14544 METHODS AND COMPOSITIONS OF HUMAN PROTEINS OF HUMAN PROTEINS OF HUMAN PRILITY OF TITLE OF INVENTION: 14544 METHODS AND COMPOSITIONS OF HUMAN PROTEINS OF HUMAN PROTEINS OF HUMAN PRILITY OF TITLE OF INVENTION NUMBER: US/11/206,587
CURRENT FILING DATE: 2005-08-18
FRIOR PELLOR DATE: 2000-11-08
FRIOR PELLOR DATE: 2000-11-08
FRIOR PELLOR DATE: 2000-11-08
FRIOR PELLOR DATE: 2000-11-08
FRIOR PELLOR DATE: 2000-11-108
FRIOR PELLOR DATE: 2000-11-15
FRIOR PERLOR PELLOR DATE: 2000-11-15
FRIOR PELLOR DATE: 2000-11-15
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US-11-201-194-5

Sequence 5, Application US/11201194

Sequence 5, Application US/11201194

Publication No. US20060019306A1

GENERAL INFORMATION:

APPLICANT: University College Cork - National University of Ireland,

APPLICANT: Cork

APPLICANT: Cork

TITLE OF INVENTION: Detection of ochratoxin A producing fungi

FILE REFERENCE: NATI25

CURRENT FILING DATE: 2005-08-11

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.2

SEQ ID NO 5

LENGTH: 582
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1 Similarity 100.0%; Pred. No. 3.6;
21; Conservative 0; Mismatches 0; Indels
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                                                                                                               Sequence 193835, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-06-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 193835

LENGTH: 25
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Fublication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION:
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT PLILING DATE: 2005-05-05
FRIOR APPLICATION NUMBER: US/05/14,294

PRIOR APPLICATION OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

LENGTH: 25

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LENGTH: 25
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100.0%; Pred. No.
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial
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US-11-136-527-193849/c
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US-10-914A-1045308/c
US-10-310-914A-1045308/c
Sequence 1045308, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: USES 10609.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 1045308
LENGTH: 20
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Monare thereof
APPLICANT: Shiler, Monare thereof
FILE REFERENCE: 06087.0200.CPUSO1
CURRENT APPLICATION UNBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 1045312
SEQ ID NO 1045312
LENGTH: 20
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100.0%; Pred. No. 11;
iive 0; Mismatches 0; Indels
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11;
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                                                                                                NAME/KEY: misc_feature

// LCCATION: (1)...(1820)

// CTHER INFORMATION: n = A,T,C or G

US-11-206-589-4
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Best Local Similarity 100.0
Matches 20, Conservative
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Best Local Similarity 100.0
Matches 20; Conservative
                                     NAME/KEY: CDS
LOCATION: (146)...(1390)
ORGANISM: Homo sapiens
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US-10-310-914A-1045312
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ORGANISM: Human
                                                                                   FEATURE:
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US-VU-3-A2-UUSA-D1303)C
Sequence 613855, Application US/09925065A
FUBLICATION NO. US2040181048A1
GENERAL INFORMATION:
APPLICATY: Wang, David G:
TITLE OF INVENTION: Naclectide Polymorphisms in the Human Genome TITLE OF INVENTION: Naclectide Polymorphisms in the Human Genome FILE REPERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR FILING DATE: 2000-10-24
FRIOR APPLICATION NUMBER: US 60/232,147
FRIOR FILING DATE: 2000-11-20
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR PILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-01-16
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12;
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PRIOR FILING DATE: 2000-11-07
PRIOR APPLICATION NUMBER: 09/284,782
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1996-11-13
PRIOR PILING DATE: 1996-11-13
PRIOR PILING DATE: 1996-11-13
SEQ ID NO SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
SENGTH: 43
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| NAME/KEY: misc_feature
| LOCATION: 481, 483, 484, 485, 486
| OTHER INFORMATION: n = A,T,C or G
| US-09-925-065A-613855
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US-11-136-527-3780/c
; Sequence 3780, Application US/11136527
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                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial
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US-09-925-065A-613855/c
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AMI01086)
FURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US/514,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 193854
LENGTH: 25
     APPLICANT: "Journ's, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 193849
LENGTH: 25
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Publication No. US20050272056A1
GENERAL INFORMATION:
APPLICANT: Quark Biotech Inc.
APPLICANT: Quark Biotech Inc.
TITLE OF INVENTION:
FILE REFERENCE: 65507-F / 003/PCT1-US4
CURRENT APPLICATION NUMBER: US/11/031,356
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 10/704,112
PRIOR APPLICATION NUMBER: 09/499,553
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1.2%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches
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US-11-136-527-193854/c
US-11-136-527-193854, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INPORMATION:
; APPLICANT: Wyeth
; APPLICANT: Woeth
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Best Local Similarity 100.0
Matches 20, Conservative
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CTHER INFORMATION: Probe
US-11-136-527-193854
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                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial
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ORGANISM: Artificial
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US-10-750-623-36767
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPRERNEE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PLING DATE: 2005-05-36
SOFTWARE PLING DATE: 2005-05-36
SOFTWARE PRIOR ENGINEER: US 60/574,294
PRIOR PLING DATE: 2005-05-05
SOFTWARE PRIOR DATE: 2005-05-05
SOFTWARE PRIOR PLING DATE: 2005-05-05
SOFTWARE PRIOR PRIOR
                                                                                                        APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 011896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin Version 3.2
SEQ ID NO 3780
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Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MI GENOMICS, INC.

APPLICANT: MENSENFELD, Sue K.

APPLICANT: RERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: RAPES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MAILO-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31
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Pred. No. 12;
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100.0%; Pred. No. 12;
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Publication No. US20050287570A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3780
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; ORGANISM: Rattus norvegicus
US-11-136-527-7876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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US-10-750-185-36767/c
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US-11-136-527-7876/c
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RESULT 66
US-11-096-568A-25683/C
US-11-096-568A-25683/C
Sequence 25683, Application US/11096568A
Sequence 25683, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NOS: 34471
LENGTH: 1280
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLB OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIII00-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 36767
LENGTH: 993
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1.2%; Score 20; DB 8; Length 993;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels
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US-10-750-623-36767/C
; Sequence 35767, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: ROSENFELD, David
: APPLICANT: ROSENFELD, David
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 36767
LENGTH: 993
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US-10-750-185-36767
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ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1280)
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Sequence 1045334
Application No. US2006003322A1
GENERAL INFORMATION:
APPLICANT:
APPLI
Sequence 1045125, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 1045325
LENGTH: 19
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
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100.0%; Pred. No. 35;
tive 0; Mismatches (
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100.0%; Pred. No. 35;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 19; Conservative
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US-10-310-914A-1045334/c
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ORGANISM: Human
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ORGANISM: Human
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Sequence 1045321, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045321
LENGTH: 19
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
NUMBER OF SEQ ID NOS: 36230
SOFTWARE: Patentin version 3.2
SEQ ID NO 3889
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100.0%; Pred. No. 13;
tive 0; Mismatches 0; Indels 0.
                                                                                                                   Length 1280;
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; OTHER INFORMATION: Ceres Seq. ID no. 13492847
US-11-096-568A-25683
                                                                                          1.2%; Scc...
100.0%; Pred. No. 12...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3889, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
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                                                                                                     Query Match
Best Local Similarity 100.
Matches 20, Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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US-10-310-914A-1045321/c
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US-10-310-914A-1045325/c
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US-11-136-527-3889
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                                                                                                                                                                                                                     APPLICANT: Characteria Angela APPLICANT: Khvorova, Anaetasia APPLICANT: Reynolds, Angela APPLICANT: Reynolds, Angela APPLICANT: Responds, Angela APPLICANT: Responds, Angela APPLICANT: Marshall, William APPLICANT: Marshall, William APPLICANT: Scarings, Stephen TITLE OF INVENTION: Functional and Hyperfunctional siRNA FILE REFREENT APPLICATION NUMBER: US/11/101,244

CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430755
LENGTH: 19
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APPLICANT: Khorova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Resholds, Angela
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Punctional and Hyperfunctional siRNA
ITILE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2003-00-0
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-11-14
SOFTWARE: Proprietary
SEQ ID NOS: 1591911
SEQ ID NO 1430756
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Pred. No. 35;
9; Mismatches 0; Indels
                                                                                                                                       Sequence 1430755, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
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  1 UCAAAGGCAUCCCUGUGUA 19
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Best Local Similarity 52.6%;
Matches 10; Conservative
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US-11-101-244-1430755
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CORGANISM: Homo sapiens
US-11-101-244-1430756
                                                                                                                 US-11-101-244-1430755
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich. Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses threeoff
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT PELLION: PUNGER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430754
LENGTH: 19
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100.0%; Pred. No. 35;
tive 0; Mismatches 0; Indels
                                                                    Score 19; DB 8; Length 19;
Pred. No. 35;
                                                                                                                 0; Indels
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100.0%; Pred. No. --.
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                                                                                                                                                          1203 GCCAGGCCCAGCTGCCACA 1221
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
                                                             Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 84.29
Matches 16; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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US-10-310-914A-1045335/c
; ORGANISM: Human
US-10-310-914A-1045334
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US-11-101-244-1430754
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ORGANISM: Human
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LENGTH: 19
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Sequence 1430760, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Characon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Marball, William
APPLICANT: Marball, William
APPLICANT: Marball, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-00-07
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430760
LENGTH: 19
Sequence 1440759, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: DEMACON, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respends, Stephen
ITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PELING DATE: 2003-09-10
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 2002-11-14
SOFTWARE: PROPILECATY
SOFTWARE: PROPILECATY
SEQ ID NOS: 1591911
SEQ ID NO 4430759
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Pred. No. 35;
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84.2%;
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Best Local Similarity 84.24
Matches 16; Conservative
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Matches 14; Conservative
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US-11-101-244-1430759
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                      | Sequence 1430757, Application US/11101244
| Sequence 1430757, Application US/11101244
| Publication No. US2050246794A1
| GENERAL INFORMATION:
| APPLICANT: Dhromacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Marball, William
| APPLICANT: Marball, William
| APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA
| FILE REFERENCE: 13499US
| CURRENT APPLICATION NUMBER: US/11/101,244
| CURRENT FILING DATE: 2003-09-10
| PRIOR PILING DATE: 2003-09-10
| PRIOR PILING DATE: 2003-09-10
| PRIOR FILING DATE: 2003-11-14
| NUMBER OF SEQ ID NOS: 1591911
| SEQ ID NO 1430757
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APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Barball, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
CURRENT APPLICATION NUMBER: 05/10/200
PRIOR PLILING DATE: 2005-04-07
PRIOR PLILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430758
LENGTH: 19
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Matches 15; Conservative
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US-11-101-244-1430758
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Best Local Similarity
Matches 15; Conserv
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US-11-101-244-1430758
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US-11-101-244-1430761

i Sequence 1430764, Application US/11101244

i Publication No. US20050246794A1

i GENERAL INFORMATION:

i APPLICANT: Bharmacon, Inc.

i APPLICANT: Revnova, Anastasia

APPLICANT: Revnova, Manstasia

APPLICANT: Resmall, William

APPLICANT: Scaringe, Stephen

ITILE OF INVENTION: Punctional and Hyperfunctional siRNA

FILE REFREENCE: 134990ER: US/11/101,244

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2003-09-107

PRIOR PILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH: 19

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"WORTH: 19
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TTTLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA; ORGANISM: Homo sapiens
US-11-101-244-1430762
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US-11-101-244-1430761
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| Subject | Subj
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APPLICANT: Characon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Restinge, Stephen
APPLICANT: Marshall, William
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
SOFTWARE: PROPRIECANT
SEQ ID NOS: 1591911
SEQ ID NO 1430764
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Pred. No. 35;
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Publication No. US20050246794A1
GENERAL INFORMATION:
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AGUAAGGAGUUAGGCAUUA 19
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-101-244-1430763
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RESULT 84

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Sequence 1430767, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
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Best Local Similarity 57.9%;
Matches 11; Conservative
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US-11-101-244-1430768
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CORGANISM: Homo sapiens
US-11-101-244-1430767
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US-11-101-244-1430765

Sequence 1430765, Application US/11101244

PUDLICATION NO. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Datamacon, Inc.

APPLICANT: Revnoids, Angela

APPLICANT: Revnoids, Angela

APPLICANT: Revnoids, Angela

APPLICANT: Leake, Devin

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFREERENT 13499BE: US/11/101,244

CURRENT FILING DATE: 2005-04-07

PRIOR FILING DATE: 2005-04-07

PRIOR FILING DATE: 2005-04-07

PRIOR FILING DATE: 2005-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1430765

LENGTH: 19
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Sequence 1430766, Application US/11101244

PUBLICATE ON O. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Marchania, Angela

APPLICANT: Leake, Devin

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Mangla

APPLICANT: Marchania miniam

APPLICANT: Lake

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-09-10

PRIOR PLING DATE: 2003-11-14

SOFTWARR: PROPRICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2003-11-14

SOFTWARR: PROPRICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2003-09-10

SOFTWARR: PROPRICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2003-09-10

SOFTWARR: PROPRICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2003-09-10
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Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Best Local Similarity 68.4%;
Matches 13; Conservative
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US-11-101-244-1430766
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US-11-101-244-1430765
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LENGTH: 19
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RESULT 86 US-11-101-244-1430767

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; Sequence 1430768, Application US/11101244
; Sequence 1430768, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Chyorova, Anstasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leakolds, Angela
; APPLICANT: Leakolds, Angela
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.1%; Score 19; DB 10; Length 19; Best Local Similarity 73.7%; Pred. No. 35; Matches 14; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshiliam
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 10;
Pred. No. 35;
8; Mismatches 0
                                                                                                                                    TILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
LENGTH: 19
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR PLILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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US-11-101-244-1430769
; Sequence 1430769, Application US/11101244
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; ORGANISM: Homo sapiens
US-11-101-244-1430771
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US-11-101-244-1430772
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                                                           APPLICANT: Khorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Acatinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: 06/502,050
PRIOR PLING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 10; Length 19;
Pred. No. 35;
2; Mismatches 0; Indels
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APPLICANT: Khyozova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPRENCE: 13499US
CURRENT FILING DATE: 2005-04-07
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1430770, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
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US-11-101-244-1430771
; Sequence 1430771, Application US/11101244
; Publication No. US20050246794A1
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Best Local Similarity 89.5%;
Matches 17; Conservative
Publication No. US20050246794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens
US-11-101-244-1430769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430770
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US-11-101-244-1430770
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LENGTH: 19
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APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILLING DATE: 2005-04-07
PRIOR PILLING DATE: 2003-09-10
PRIOR PILLING DATE: 2003-09-10
PRIOR PILLING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NOS: 1591911
SEQ ID NO 1430772
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PLING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430771
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. 35;
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Pred. No. 35;
3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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Pred. No.
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Edworova, Inc.
APPLICANT: Rivorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-101-244-1430773
; Sequence 1430773, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Gaps
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Bublication No. US20050246794A1

GENERAL INPORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-010

PRIOR PILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SEQ ID NO 1430776

LENGTH: 19
  APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPRENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430775
LENGTH: 19
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Pred. No. 35;
9; Mismatches 0; Indels
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Matches 16; Conservative 3; Mismatcher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1235 AAGCATGGCCTACAGAATG 1253
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1 CUGAUGUUCUGUAUCUUAA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.61
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Homo sapiens
US-11-101-244-1430776
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US-11-101-244-1430777
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; Sequence 1430774, Application US/11101244
; Publication No. US202050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Marchall, William
; APPLICANT: Marchall, William
; APPLICANT: Marchall, William
; APPLICANT: Marchall, William
; PRICANT: Marchall, William
; PRICANT: Marchall, William
; PRICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/520,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SEQ ID NO 1430774
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolda Angela
APPLICANT: Reynolda Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR FILING DATE: 2003-09-10
FRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430773
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 10; Length 19;
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 19; DB 10; Length 19; 78.9%; Pred. No. 35;
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1430773
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US-11-101-244-1430775
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US-11-101-244-1430774
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Sequence 1430781, Application US/11101244

Sequence 1430781, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Bearen, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Bearen, Devin

APPLICANT: Scatinge, Stephen

ITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REPERENCE: 13499US

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2005-04-07

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH: 19
           APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 19;
35;
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Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1609 GCAGGGCCCACTCTATGTT 1627
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Reynolds, Angela
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Best Local Similarity 63.2%;
Matches 12; Conservative
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Best Local Similarity 73.73
Matches 14, Conservative
Leake, Devin
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                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-101-244-1430780
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; ORGANISM: Homo sapiens
US-11-101-244-1430781
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                                                                                                                                                                                                                                                                           SEQ ID NO 1430780
LENGTH: 19
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         APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marehall, William
APPLICANT: Scaringe, Stephonal
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1430777
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Khorova, Anastasia
APPLICANT: Khorova, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marbhall, William
APPLICANT: Marbhall, William
APPLICANT: Marchall, William
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1430778
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 10; Length 19;
Pred. No. 35;
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89.5%; Pred. No. 35;
ive 2; Mismatches 0; Indele
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Charmacon, Inc.
APPLICANT: Kivorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1430778, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1635 GGAGTTGGTTCTGGTTCTT 1653
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                                                                                                                                                                                                                                                                                                                                           ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430777
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Best Local Similarity
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Matches 17; Conserv
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US-11-101-244-1430778
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US-11-101-244-1430780
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